	MS-GPC-8-27-7	MS-GPC-8-27-10	MS-GPC-8-6-13	MS-GPC-8-27-41	MS-GPC-8-6-47	MS-GPC-8-10-57	MS-GPC-8-6-27	MS-GPC-8	MS-GPC-8-6
Plastic	-0.004	-0.020	-0.022	-0.025	-0.001	0.005	0.007	-0.022	-0.018
BSA	-0.003	-0.019	-0.021	-0.022	0.008	0.003	0.003	-0.016	-0.019
Testosterone -BSA	-0.005	-0.010	-0.012	-0.007	0.011	0.003	0.002	-0.009	-0.012
Lysozyme	-0.005	-0.079	-0.079	-0.073	0.013	0.014	0.006	-0.081	-0.072
human Apotransferrin	-0.009	-0.016	-0.018	-0.018	-0.005	-0.008	-0.004	-0.014	-0.016
MHCII (DRA*0101/ DRB1*0401)	1.549	1.493	1.467	1.525	1.400	1.256	1.297	1.058	1.306

Fig. 1A

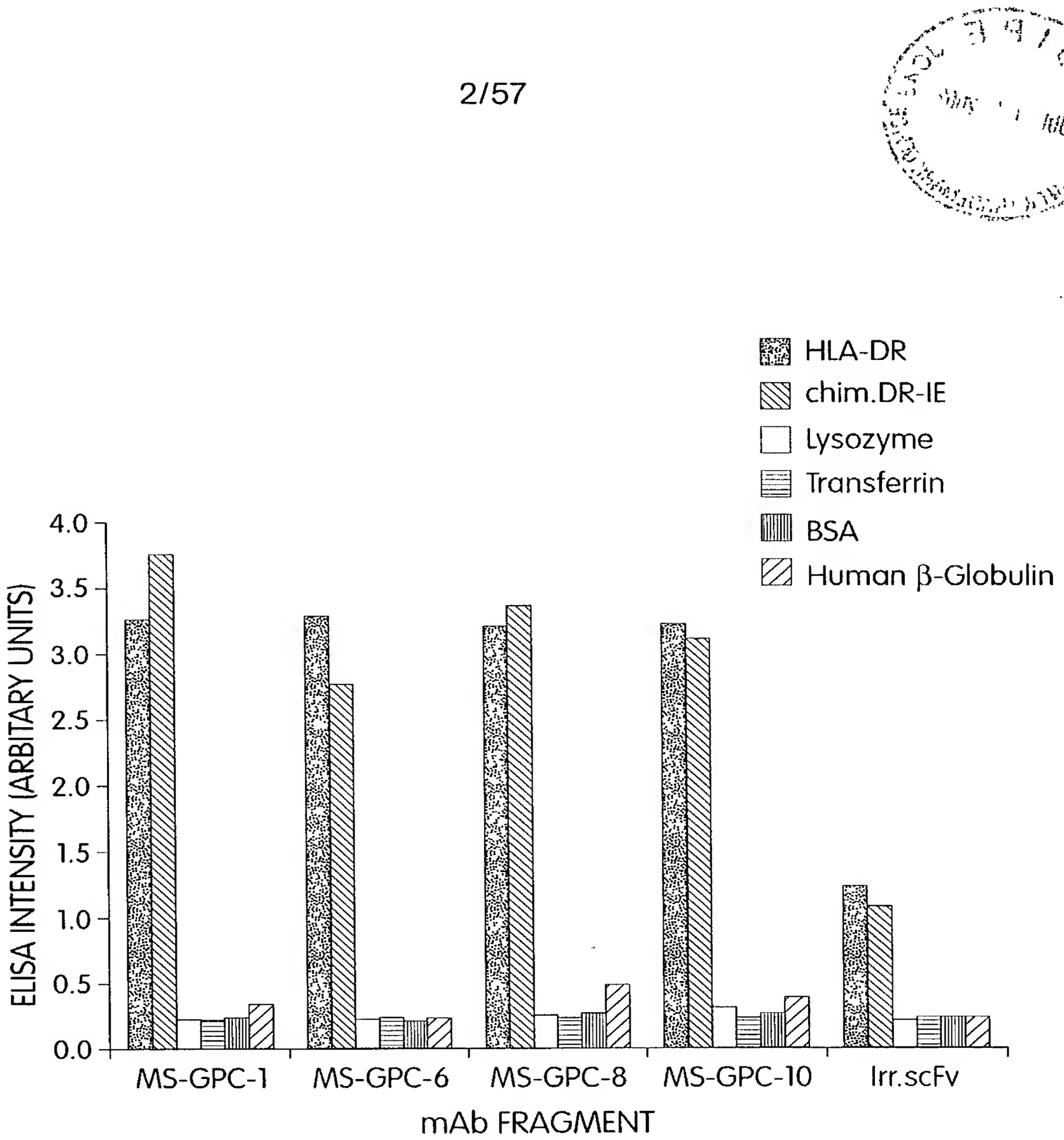
HLA-DR
chim.DR-IE
Lysozyme
Transferrin
BSA
Human β-Globulin
ELISA INTENSITY (ARBITARY UNITS)
4.0
3.5
3.0
2.5
2.0
1.5
1.0
0.5
0.0
MS-GPC-1
MS-GPC-6
MS-GPC-8
MS-GPC-10
Irr.scFv
mAb FRAGMENT

Fig. 1B

Target Proteins	scFv												IgG		
	17	2E	45	5C	73	8A	A1	B8	E6	FD	159	170	1D09C3	1C7277	305D3
DR4Dw4 Purified	+[a]	+	+	+	+	+	+	+	+	+	+	+	+	+	+
Chimeric DR-IE purified	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+
Lysozyme	-[b]	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Transferrin	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
BSA	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Human gamma globulin	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-

a. In Elisa, OD (at 370 nm - background): > 1.5

b. In Elisa, OD (at 370 nm - background): < 0.5

Fig. 1C

Cell Line	HLA-	DRB1*	scFv												IgG		
			17	2E	45	5C	73	8A	A1	B8	E6	FD	159	170	1D09C3	1C7277	305D3
LG2	DR1	0101	+[a]	+	-[b]	-	+	+	+	+	+	+	+	+	+	+	+
E4181324	DR2	15021	+	+	-	-	+	+	+	+	+	+	+	+	+	+	+
VAVY	DR3	0301	+	+	-	-	+	+	+	+	+	+	+	+	+	+	+
PRIESS	DR4Dw4	0401	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+/-[c]
TS10	DR4Dw10	0402	+	+	-	+/-	+	+	+	+	+	+	+	+	+	+	+
BIN40	DR4Dw14	0404	+	+	+	+/-	+	+	+	+	+	+	+	+	+	+	+
TAB089	DR8	8031	+	+	-	+/-	+	+	+	+	+	+	+	+	+	+	+
DKB	DR9	9012	+	+	+/-	+/-	+	+	+	+	+	+	+	+	+	+	+/-
WT47	DR13	1302	+	+	-	-	+	+	+	+	+	+	+	+	+	+	+
TEM	DR14	1401	+	+	+	+/-	+	+	+	+	+	+	+	+	+	+	+
L105.1	DRw52	B3*0101	+	-	-	-	nt[d]	+	-	+	+	+	nt	nt	+/-	+/-	+/-
L257.6	DRw53	B4*0101	+/-	-	+	-	nt	+	-	+	+/-	+/-	nt	nt	+	+	+
L25.4	DPw4/w4.2	DP0103/0402	-	-	-	-	nt	+	-	-	-	-	nt	nt	+/-	-	+/-
L256.12	DPw2/w2.1	DP0202/0201	-	-	-	-	nt	+/-	-	-	-	-	nt	nt	-	-	-
L21.3	DQ7/w2	DQ0201/0602	-	-	-	-	nt	+	-	+	-	-	nt	nt	nt	nt	nt
Target Cell			% Cells Killed[e]														
PRIESS			**75**	20	28	32	22	**89**	33	**59**	**75**	34	1	5	**88**	**93**	**74**

a. FACS analysis, mAb + FITC-anti human IgG_4, mean fluorescence intensity > 30.

b. Mean fluorescence intensity < 10.

c. Mean fluorescence intensity 10-30.

d. Not tested.

e. Based on viable cell recovery after treatment with 200nM scFv plus 100 nM anti-FLAG or 50 nM mab at 37°C for 4h. Determined by light.

Fig. 2

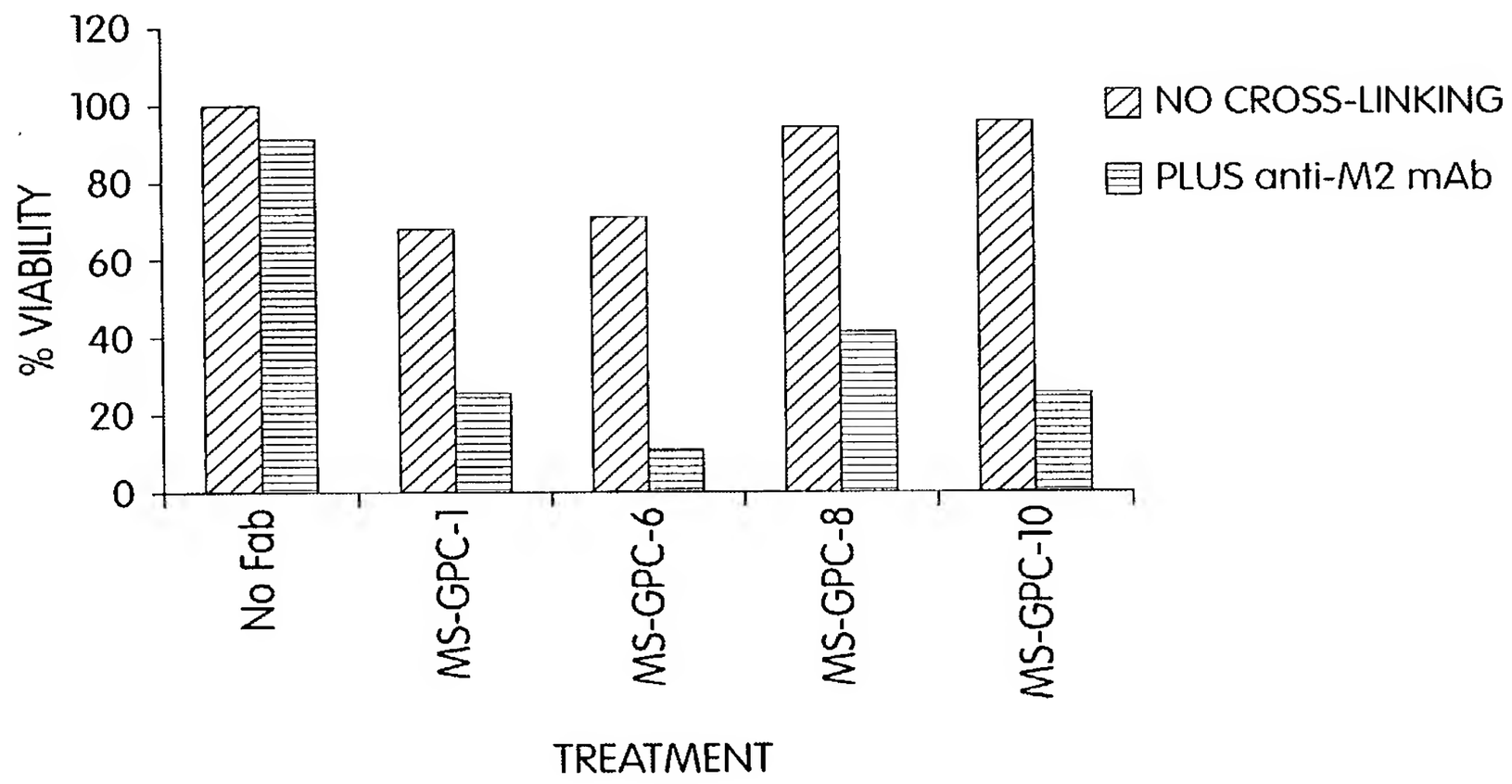
120
100
80
60
40
20
0
% VIABILITY
NO CROSS-LINKING
PLUS anti-M2 mAb
No Fab
MS-GPC-1
MS-GPC-6
MS-GPC-8
MS-GPC-10
TREATMENT

Fig. 3

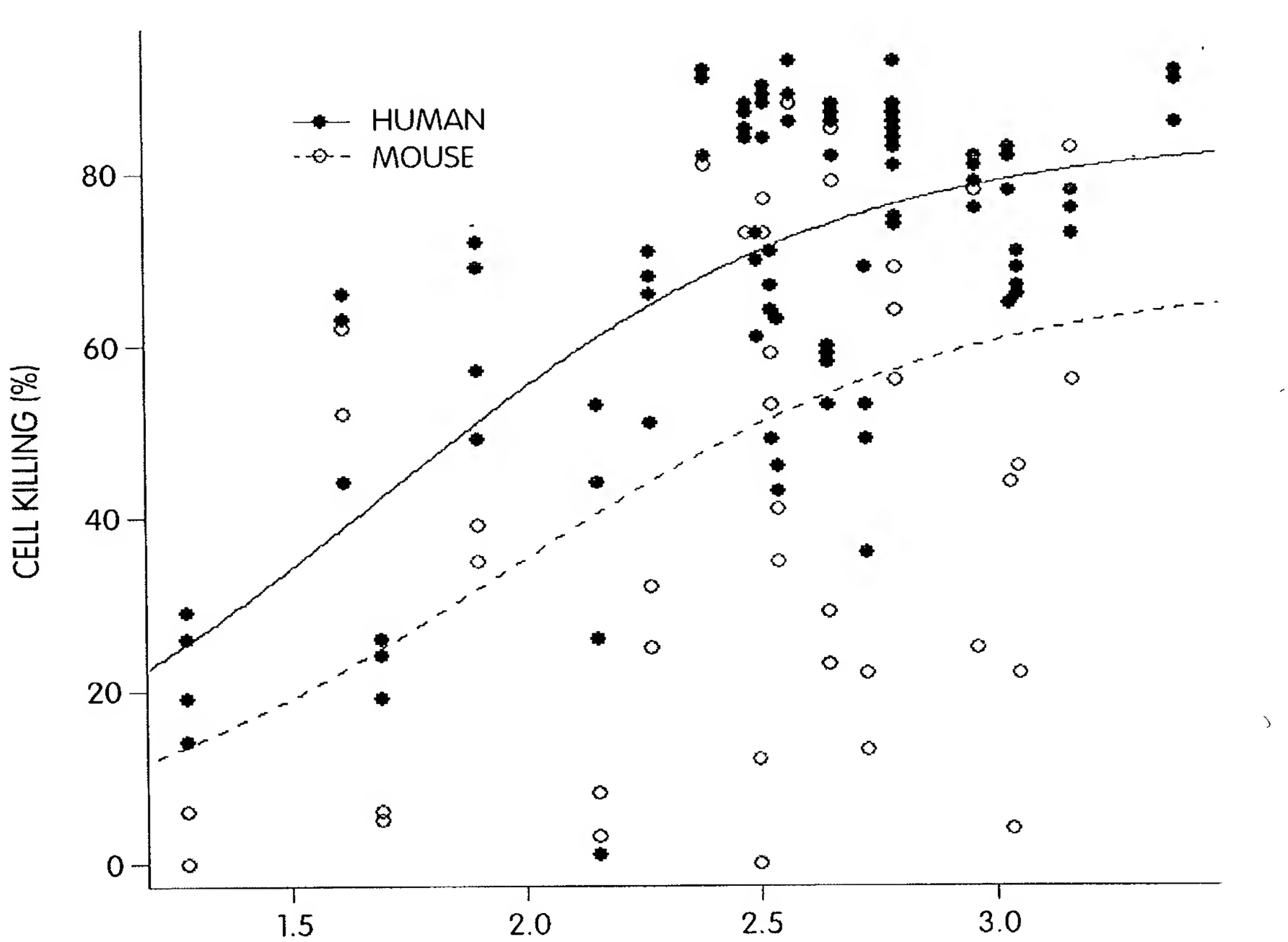
HUMAN
MOUSE
CELL KILLING (%)
0
20
40
60
80
1.5
2.0
2.5
3.0
Log10(HLA DR EXPRESSION)/ARBRITARY UNITS

Fig. 4

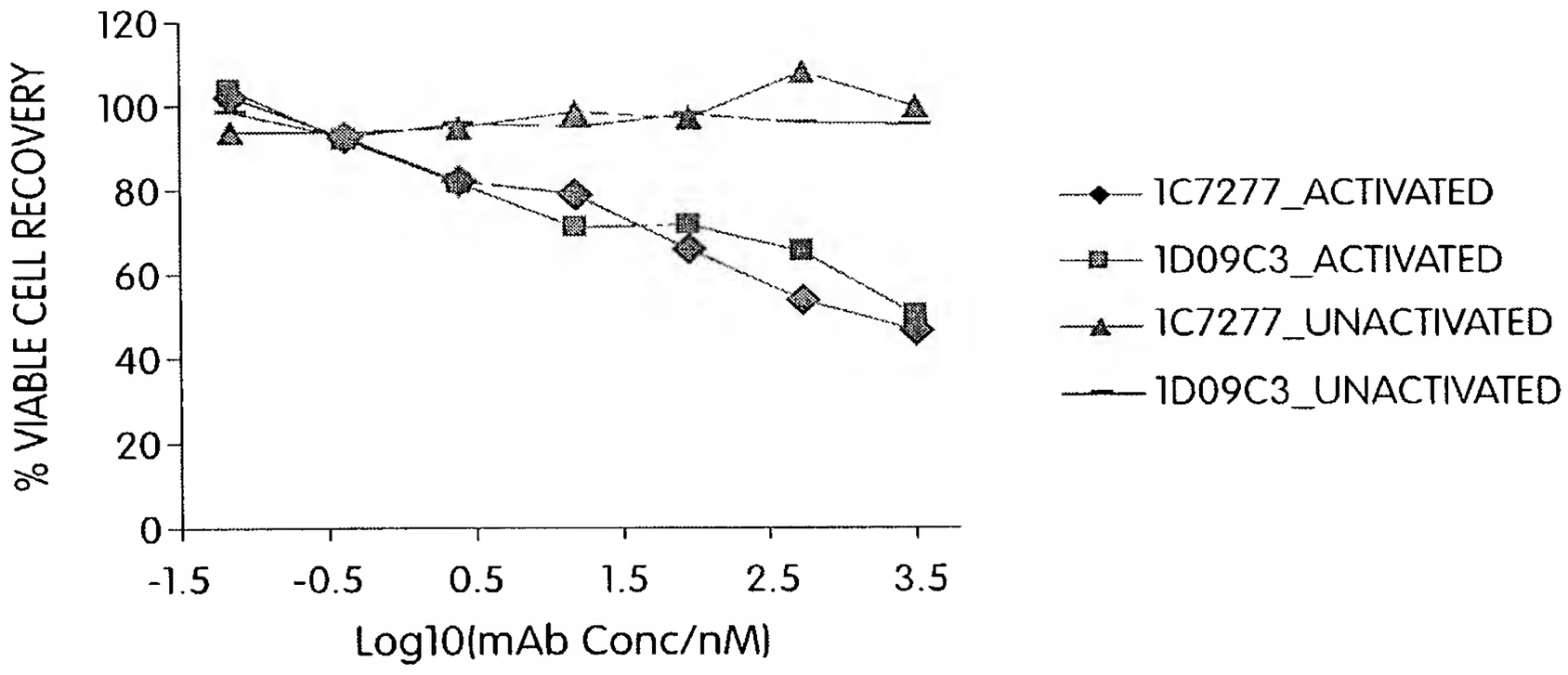
120
100
80
60
40
20
0
% VIABLE CELL RECOVERY
-1.5
-0.5
0.5
1.5
2.5
3.5
Log10(mAb Conc/nM)
1C7277_ACTIVATED
1D09C3_ACTIVATED
1C7277_UNACTIVATED
1D09C3_UNACTIVATED

Fig. 5

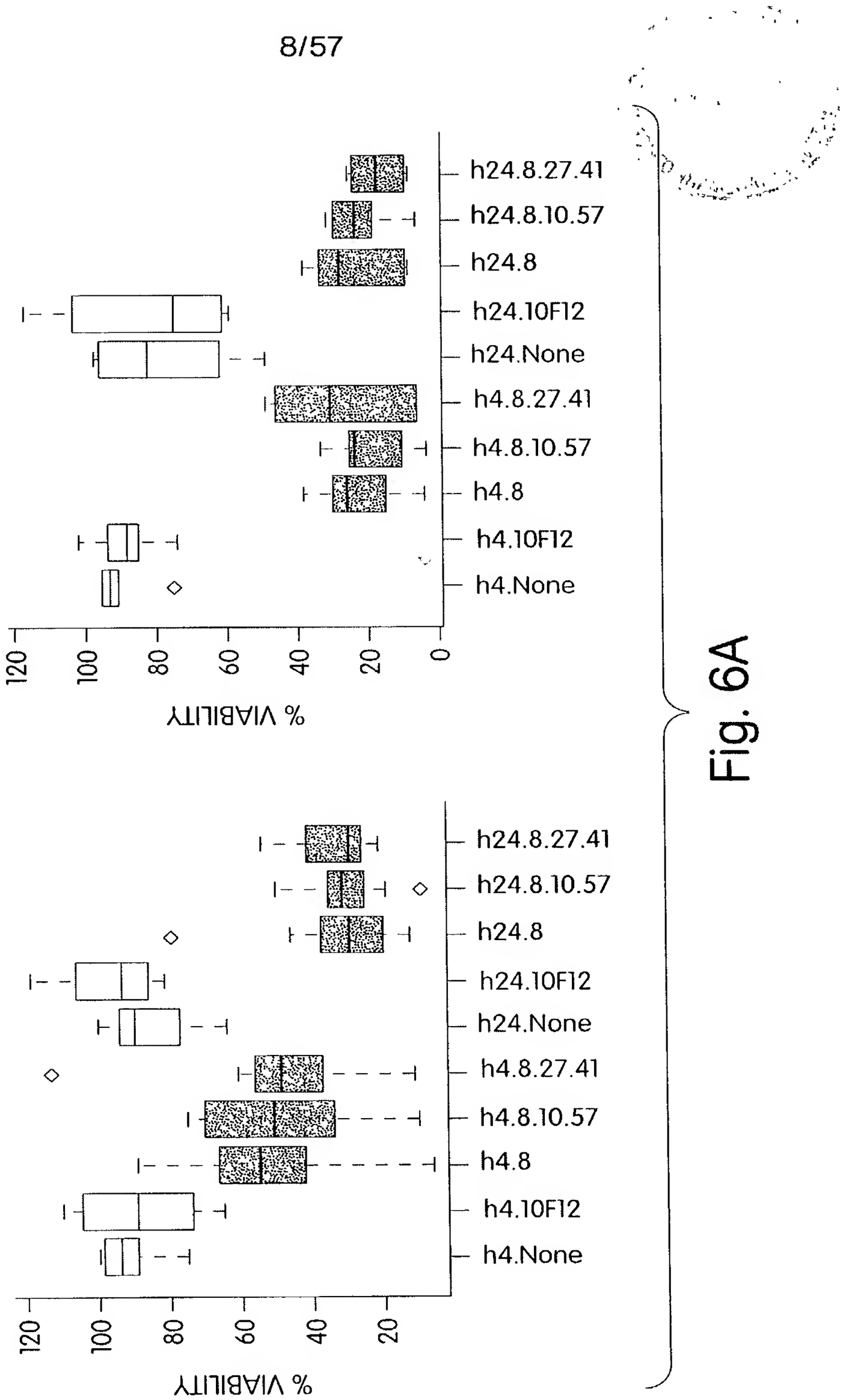
h24.8.27.41
h24.8.10.57
h24.8
h24.10F12
h24.None
h4.8.27.41
h4.8.10.57
h4.8
h4.10F12
h4.None
120
100
80
60
40
20
0
% VIABILITY
h24.8.27.41
h24.8.10.57
h24.8
h24.10F12
h24.None
h4.8.27.41
h4.8.10.57
h4.8
h4.10F12
h4.None
120
100
80
60
40
20
% VIABILITY

Fig. 6A

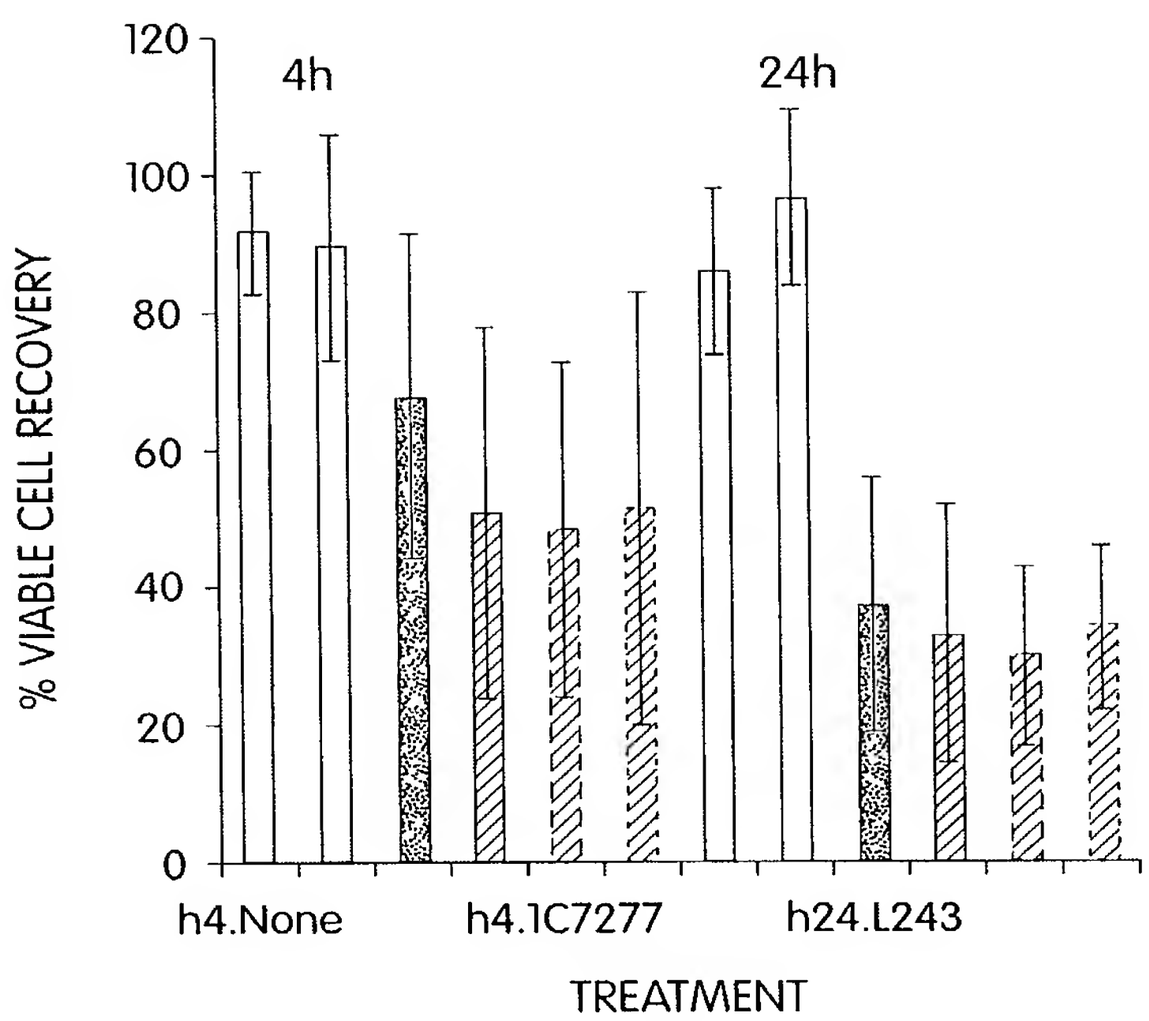
120
100
80
60
40
20
0
4h
24h
% VIABLE CELL RECOVERY
h4.None
h4.1C7277
h24.L243
TREATMENT

Fig. 6B

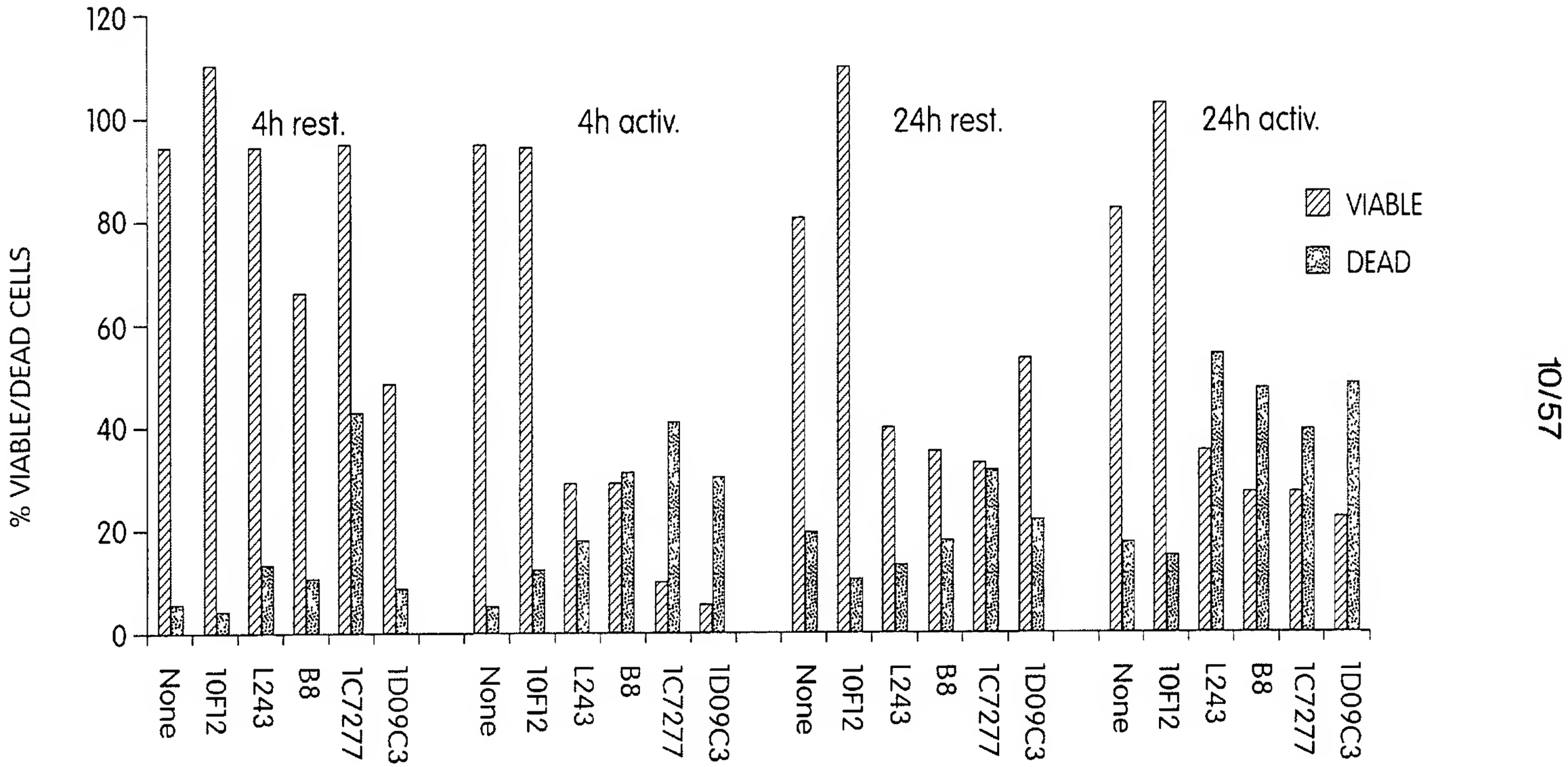
% VIABLE/DEAD CELLS
120
100
80
60
40
20
0
4h rest.
4h activ.
24h rest.
24h activ.
VIABLE
DEAD
None
10F12
L243
B8
1C7277
1D09C3

Fig. 6C

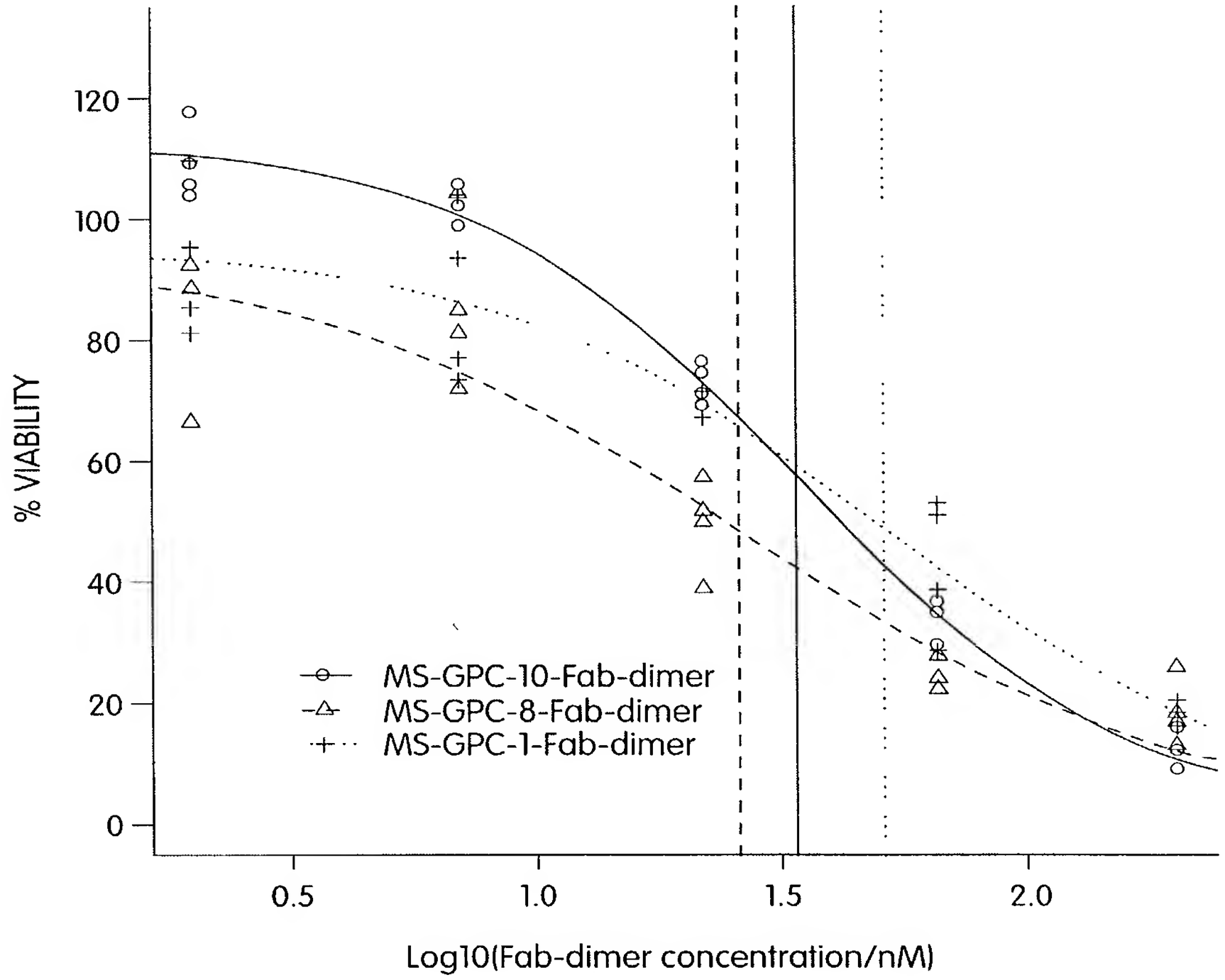
120
100
80
60
40
20
0
% VIABILITY
0.5
1.0
1.5
2.0
MS-GPC-10-Fab-dimer
MS-GPC-8-Fab-dimer
MS-GPC-1-Fab-dimer
Log10(Fab-dimer concentration/nM)

Fig. 7A

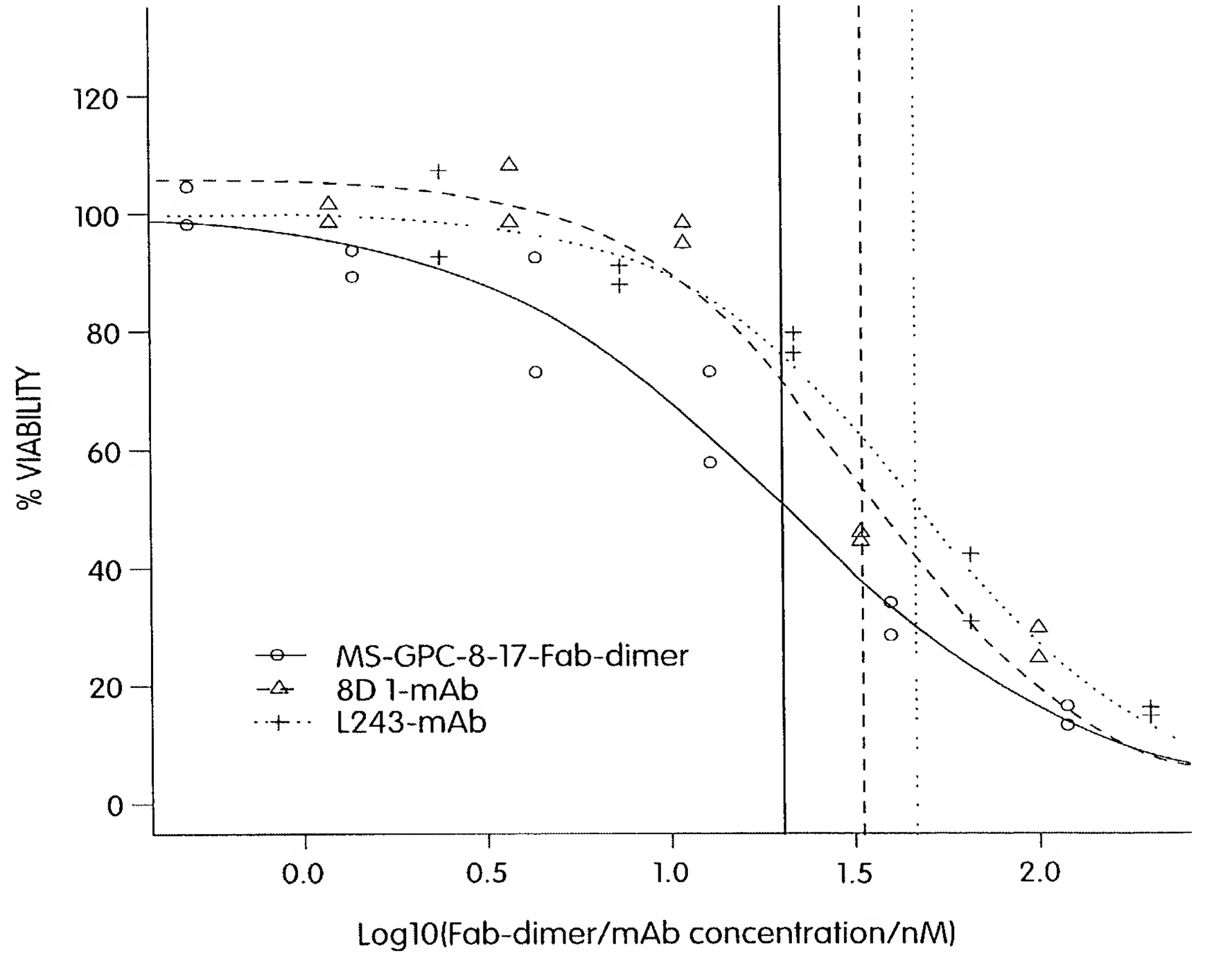
% VIABILITY
120
100
80
60
40
20
0
0.0
0.5
1.0
1.5
2.0
MS-GPC-8-17-Fab-dimer
8D 1-mAb
L243-mAb
Log10(Fab-dimer/mAb concentration/nM)

Fig. 7B

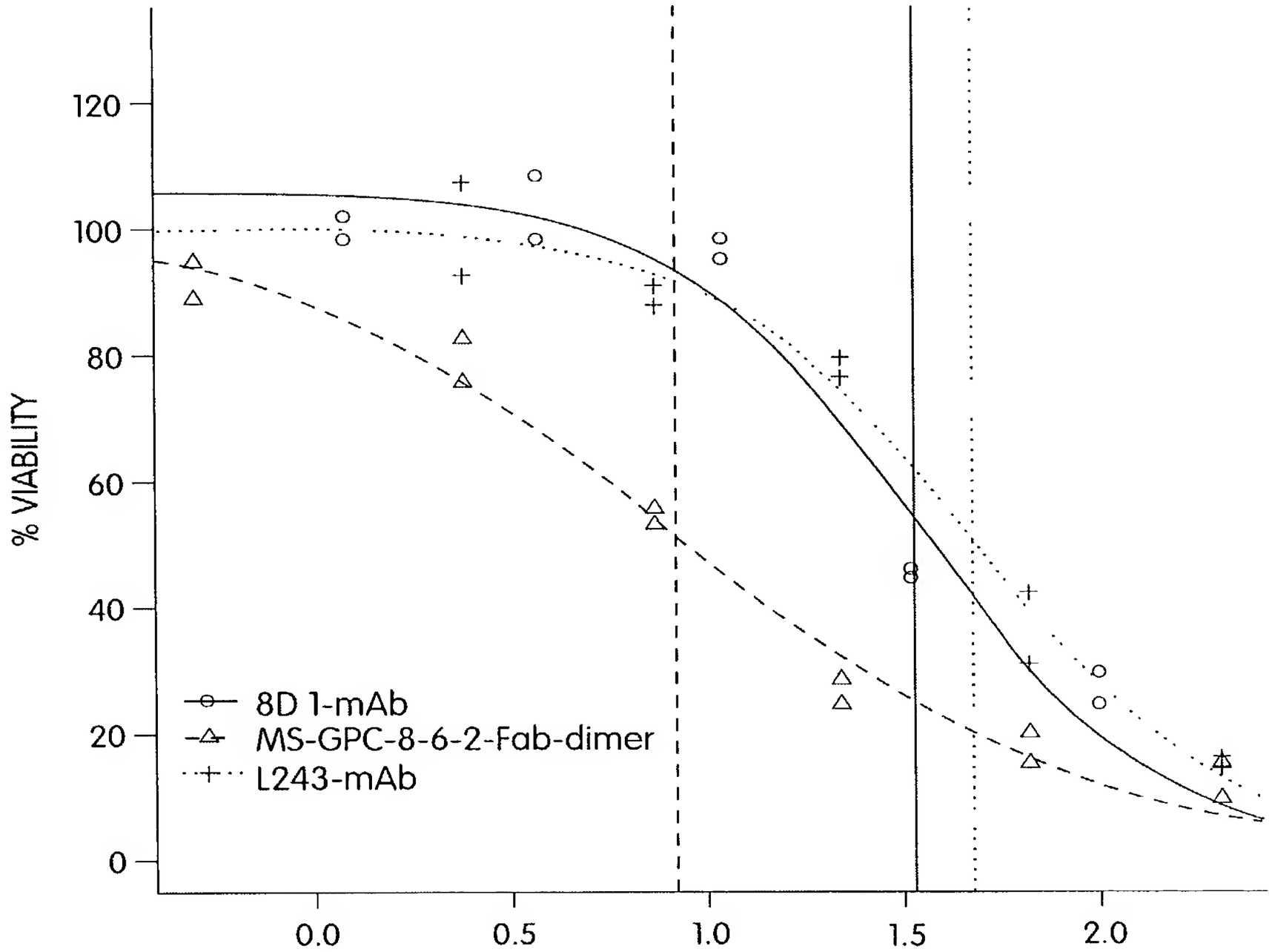
120
100
80
60
40
20
0
% VIABILITY
0.0
0.5
1.0
1.5
2.0
8D 1-mAb
MS-GPC-8-6-2-Fab-dimer
L243-mAb
Log10(Fab-dimer/mAb concentration/nM)

Fig. 7C

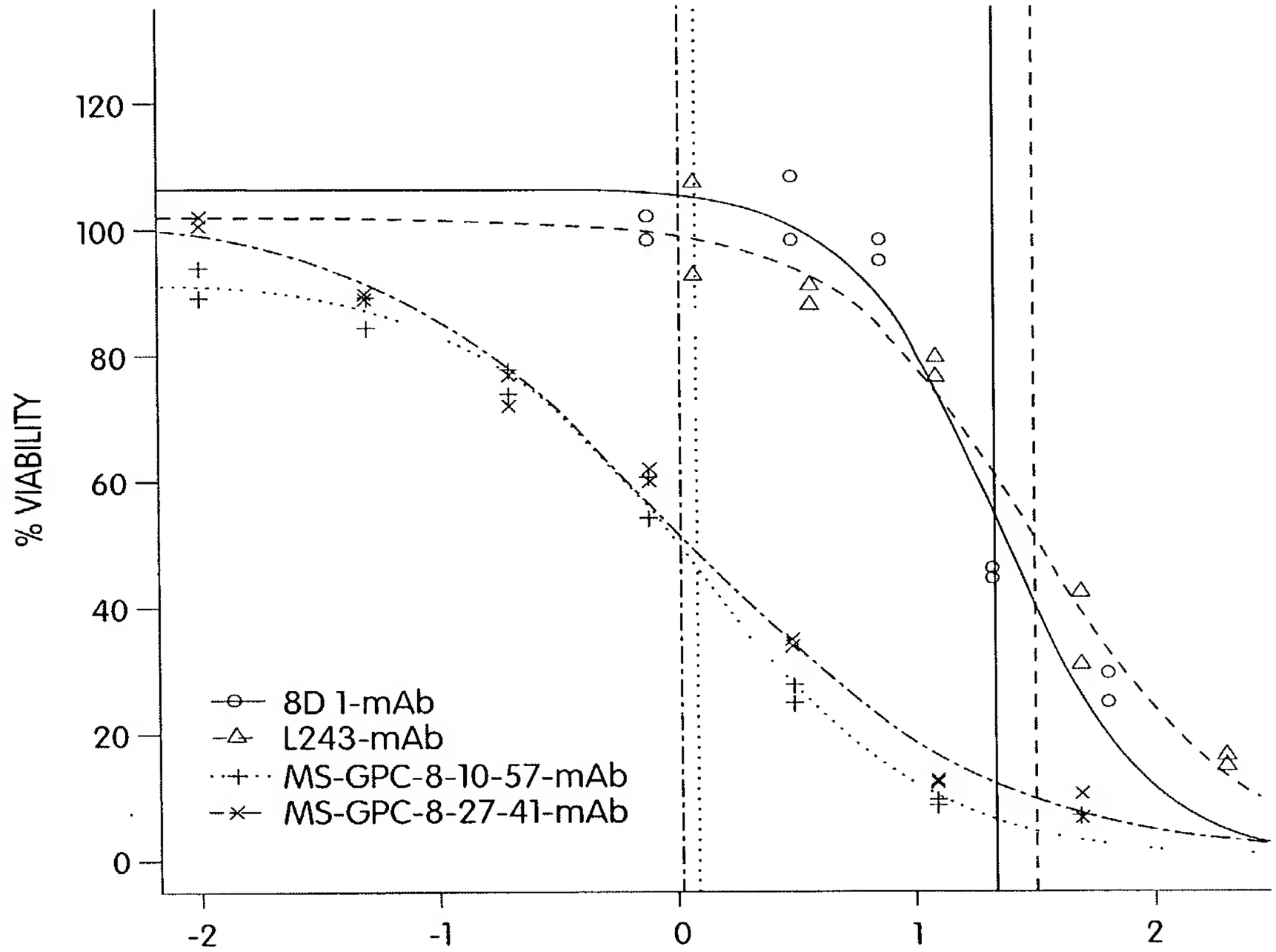
% VIABILITY
120
100
80
60
40
20
0
-2
-1
0
1
2
8D 1-mAb
L243-mAb
MS-GPC-8-10-57-mAb
MS-GPC-8-27-41-mAb
Log10(mAb concentration/nM)

Fig. 7D

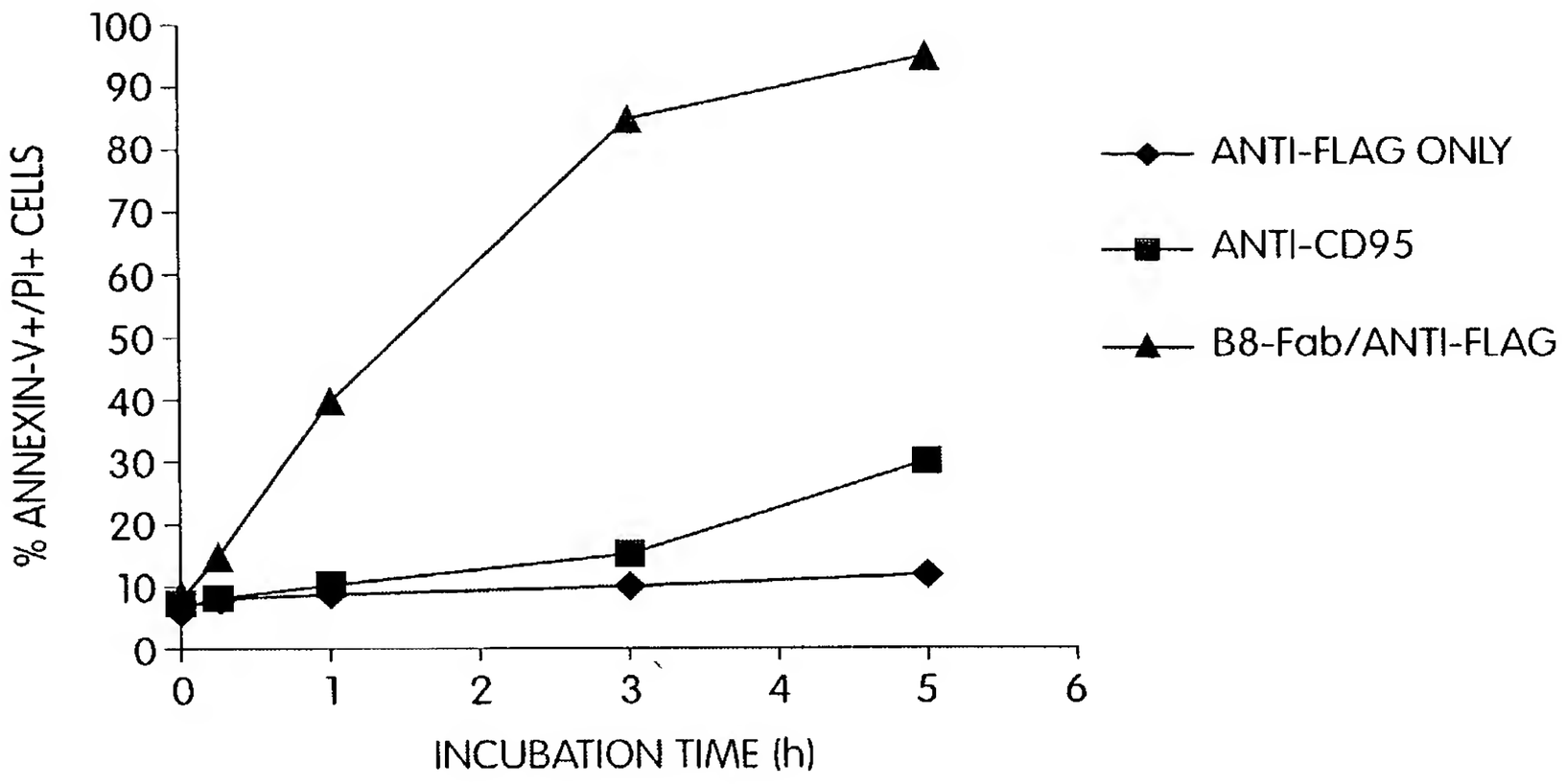
% ANNEXIN-V+/PI+ CELLS
100
90
80
70
60
50
40
30
20
10
0
0
1
2
3
4
5
6
INCUBATION TIME (h)
ANTI-FLAG ONLY
ANTI-CD95
B8-Fab/ANTI-FLAG

Fig. 8A

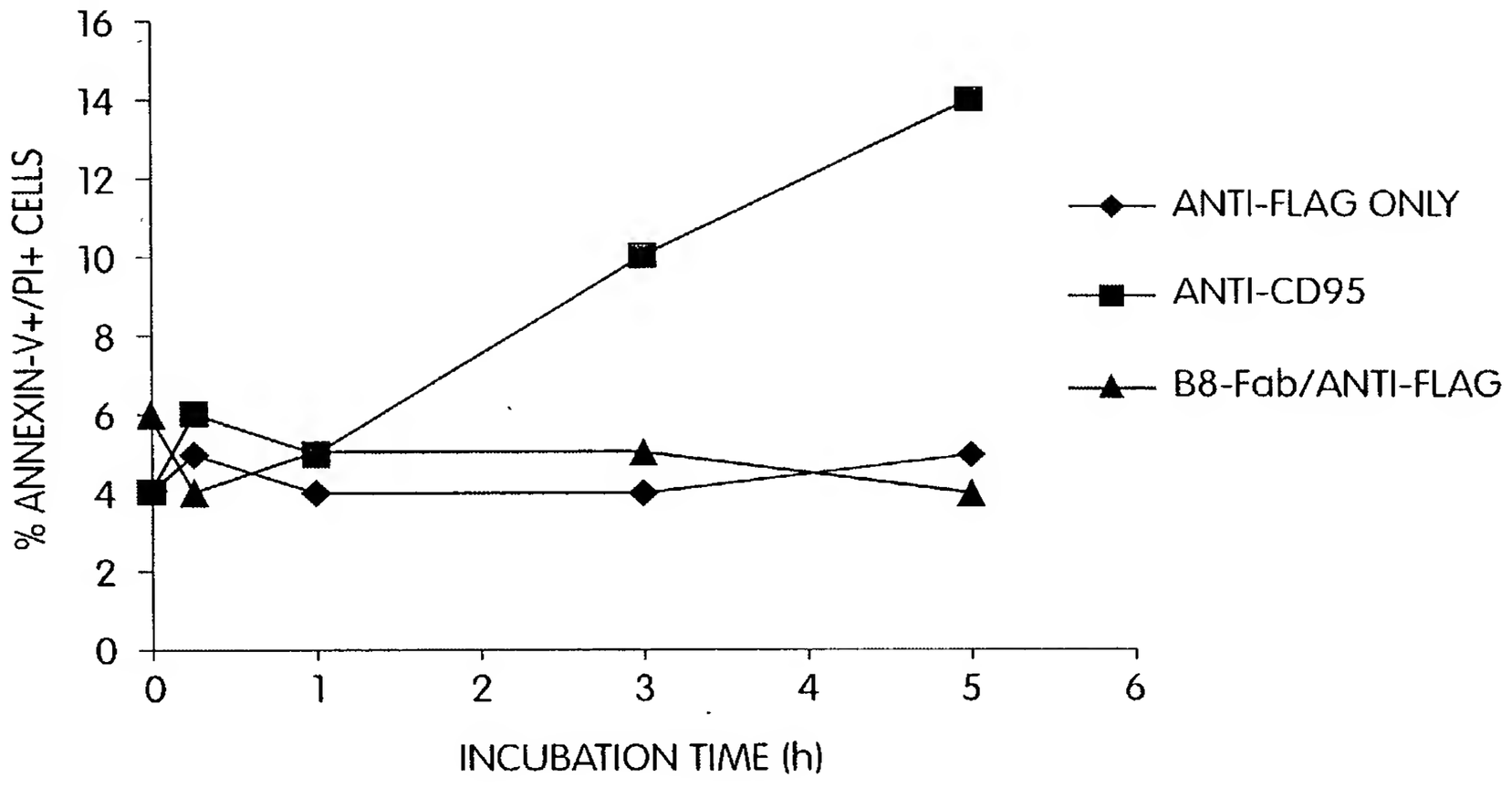
% ANNEXIN-V+/PI+ CELLS
INCUBATION TIME (h)
ANTI-FLAG ONLY
ANTI-CD95
B8-Fab/ANTI-FLAG
0
2
4
6
8
10
12
14
16
0
1
2
3
4
5
6

Fig. 8B

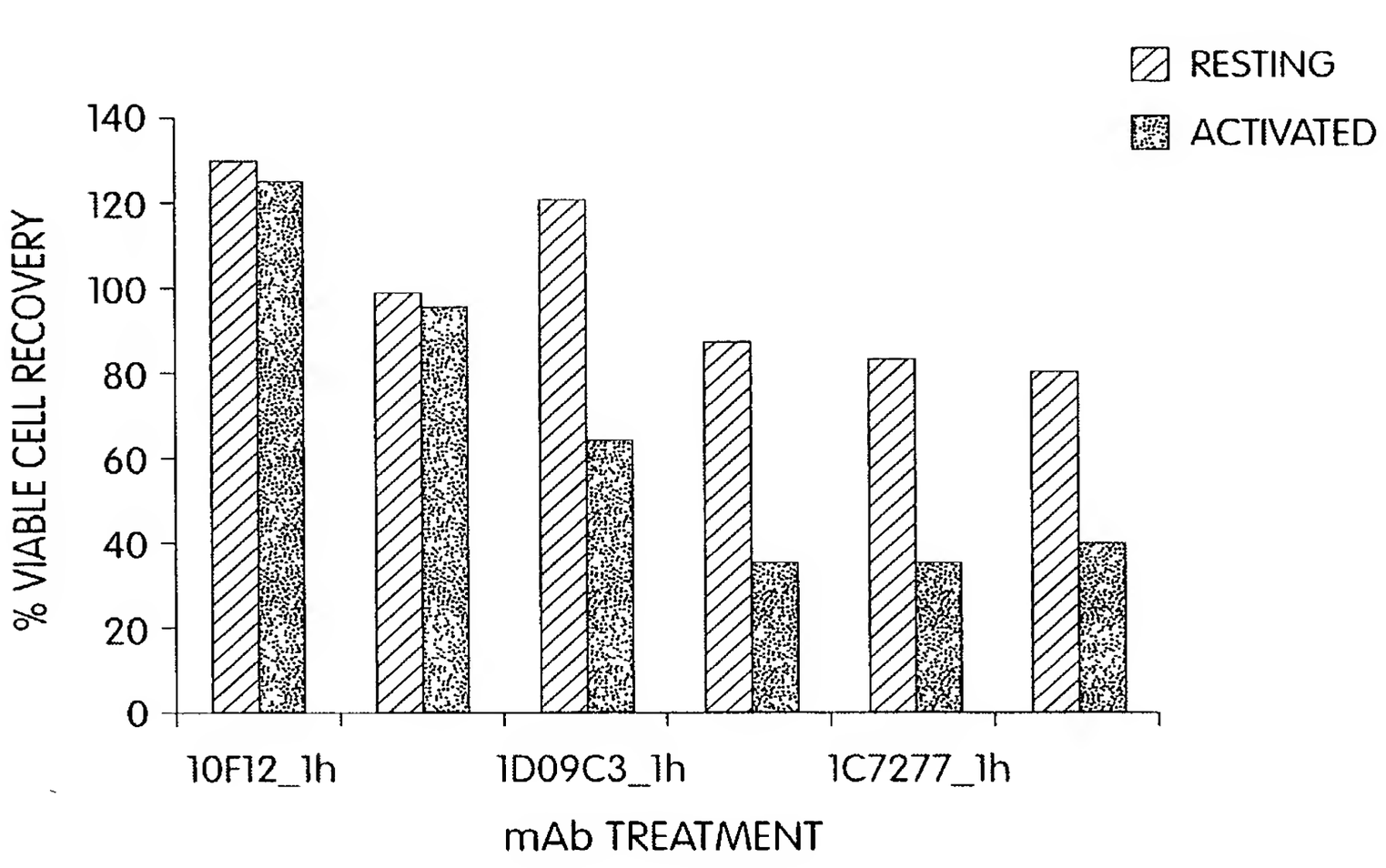
RESTING
ACTIVATED
% VIABLE CELL RECOVERY
140
120
100
80
60
40
20
0
10F12_1h
1D09C3_1h
1C7277_1h
mAb TREATMENT

Fig. 8C

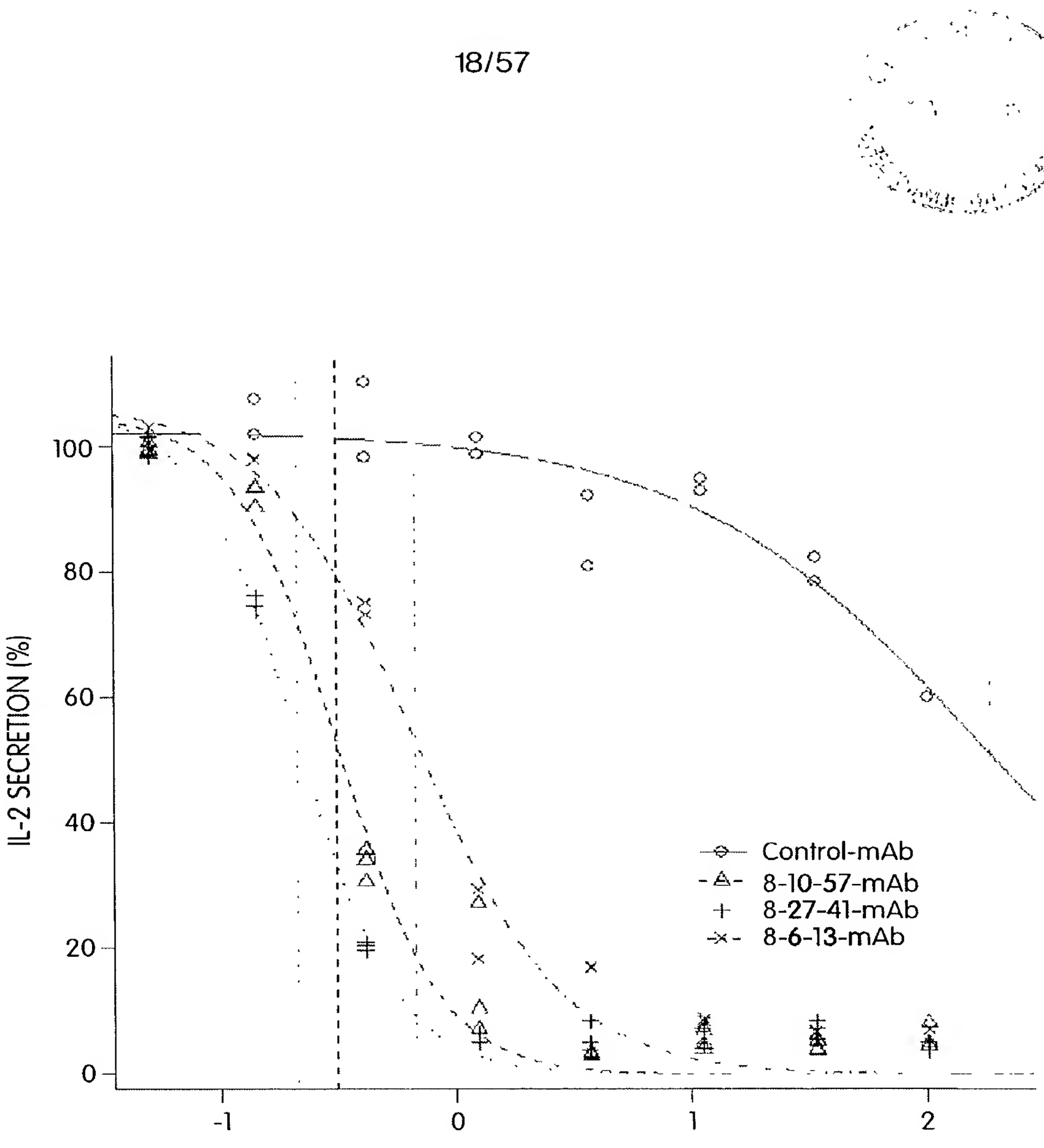
IL-2 SECRETION (%)
100
80
60
40
20
0
-1
0
1
2
Log10(mAb concentration/nM)
Control-mAb
8-10-57-mAb
8-27-41-mAb
8-6-13-mAb

Fig. 9A

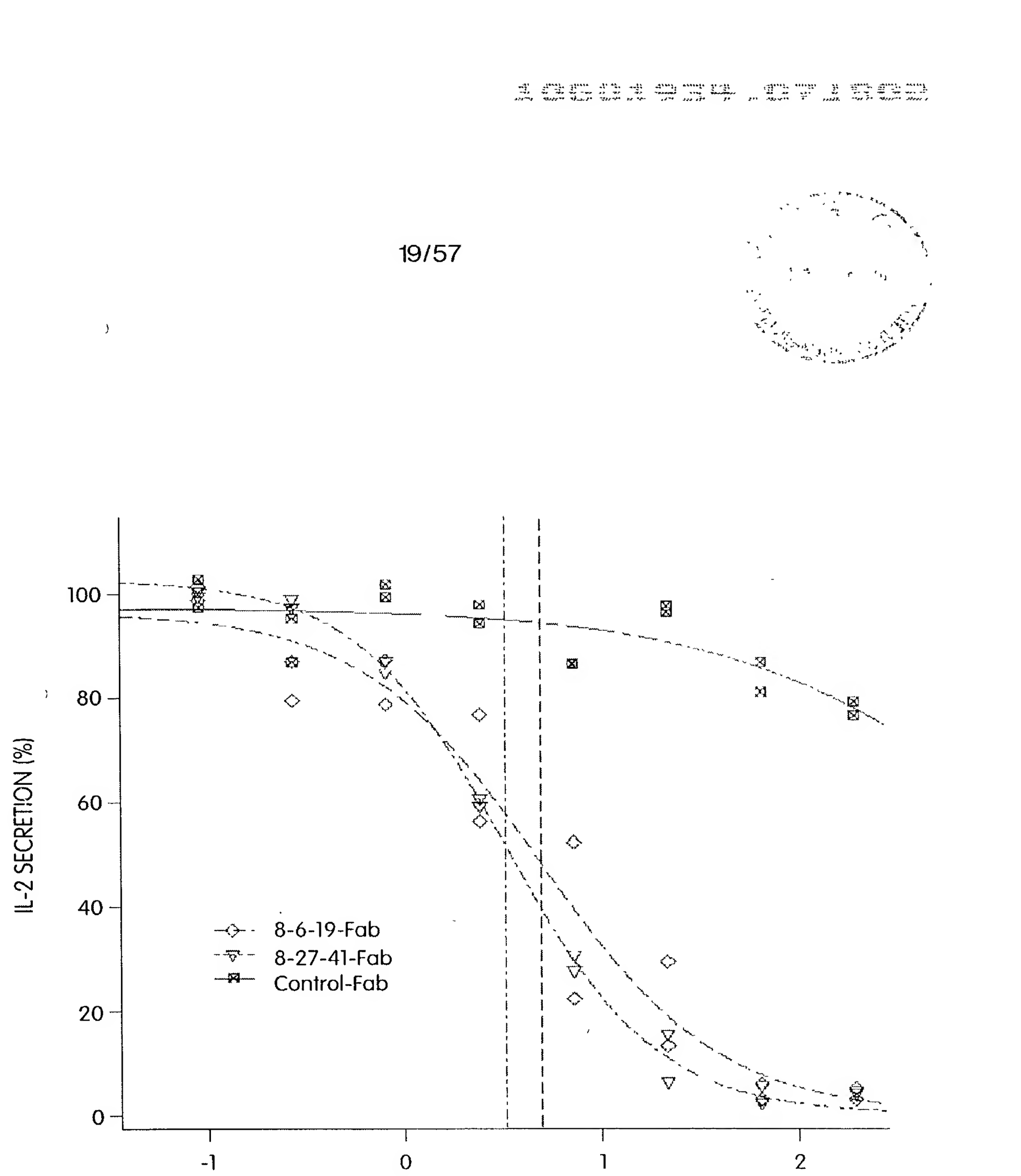
IL-2 SECRETION (%)
100
80
60
40
20
0
8-6-19-Fab
8-27-41-Fab
Control-Fab
-1
0
1
2
Log10(Fab concentration/2nM)

Fig. 9B

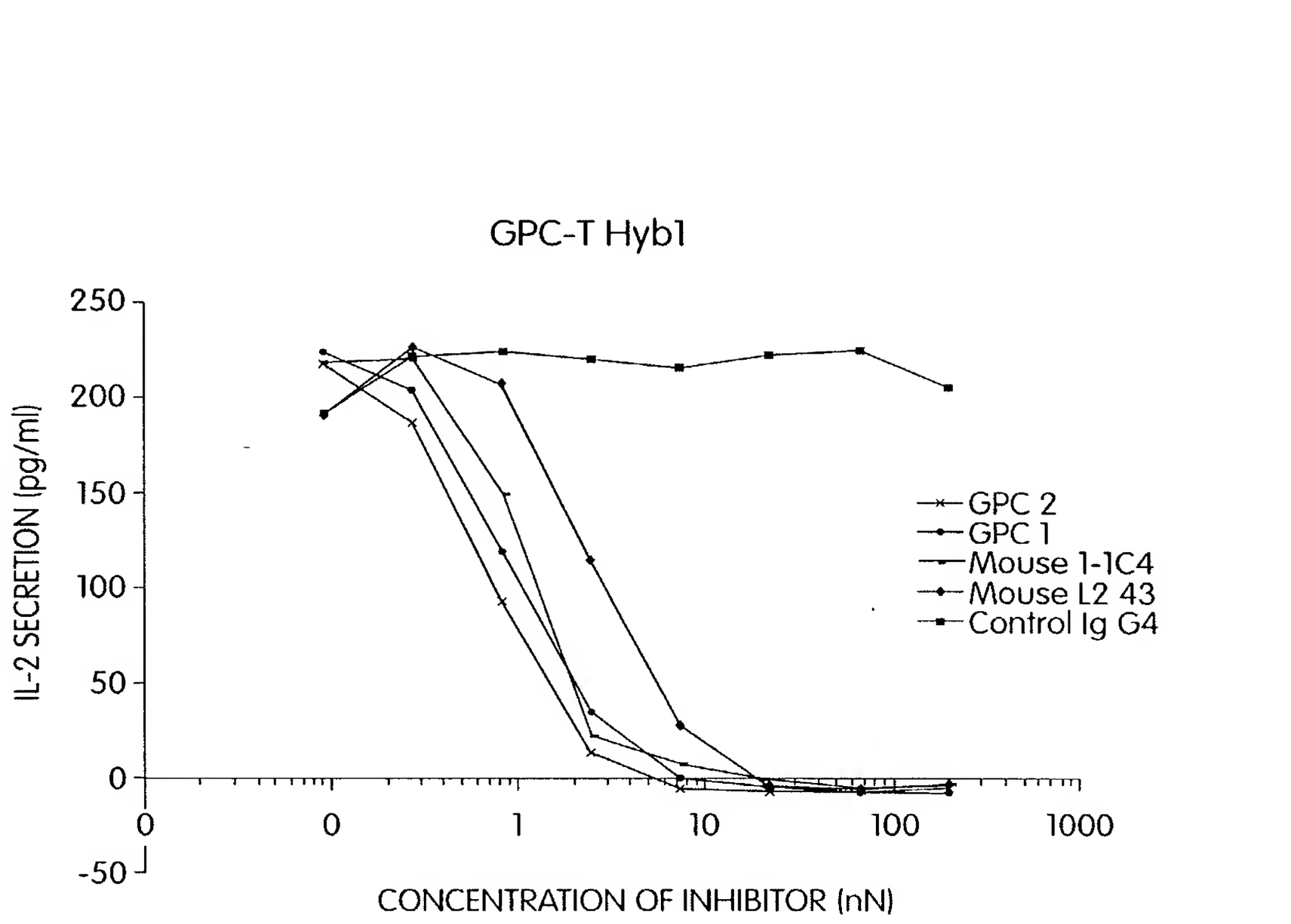
GPC-T Hyb1
250
200
150
100
50
0
-50
IL-2 SECRETION (pg/ml)
0
0
1
10
100
1000
CONCENTRATION OF INHIBITOR (nN)
GPC 2
GPC 1
Mouse 1-1C4
Mouse L2 43
Control Ig G4

Fig. 9C

Cell line NG-TcL HA-10

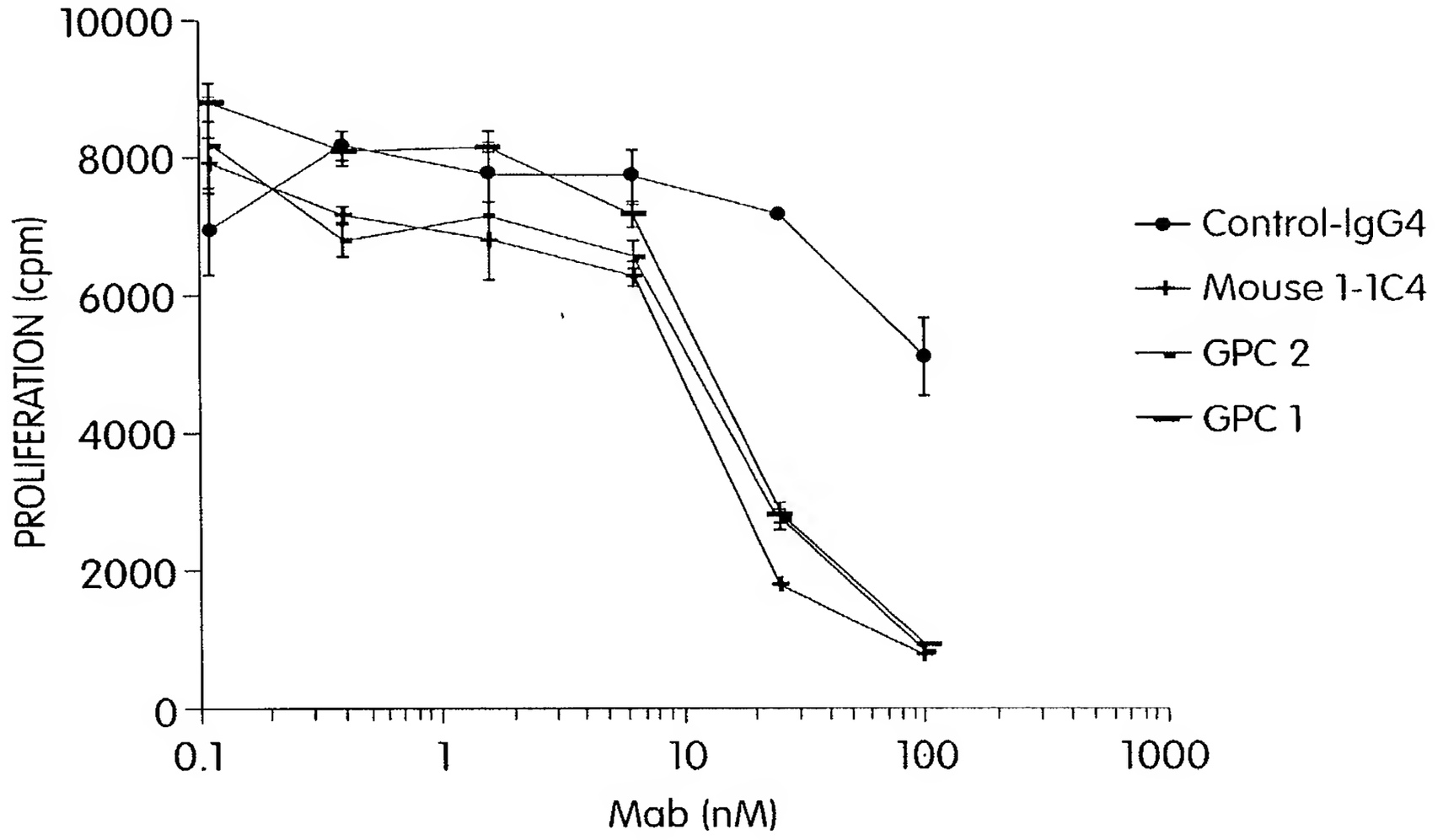

Fig. 9D

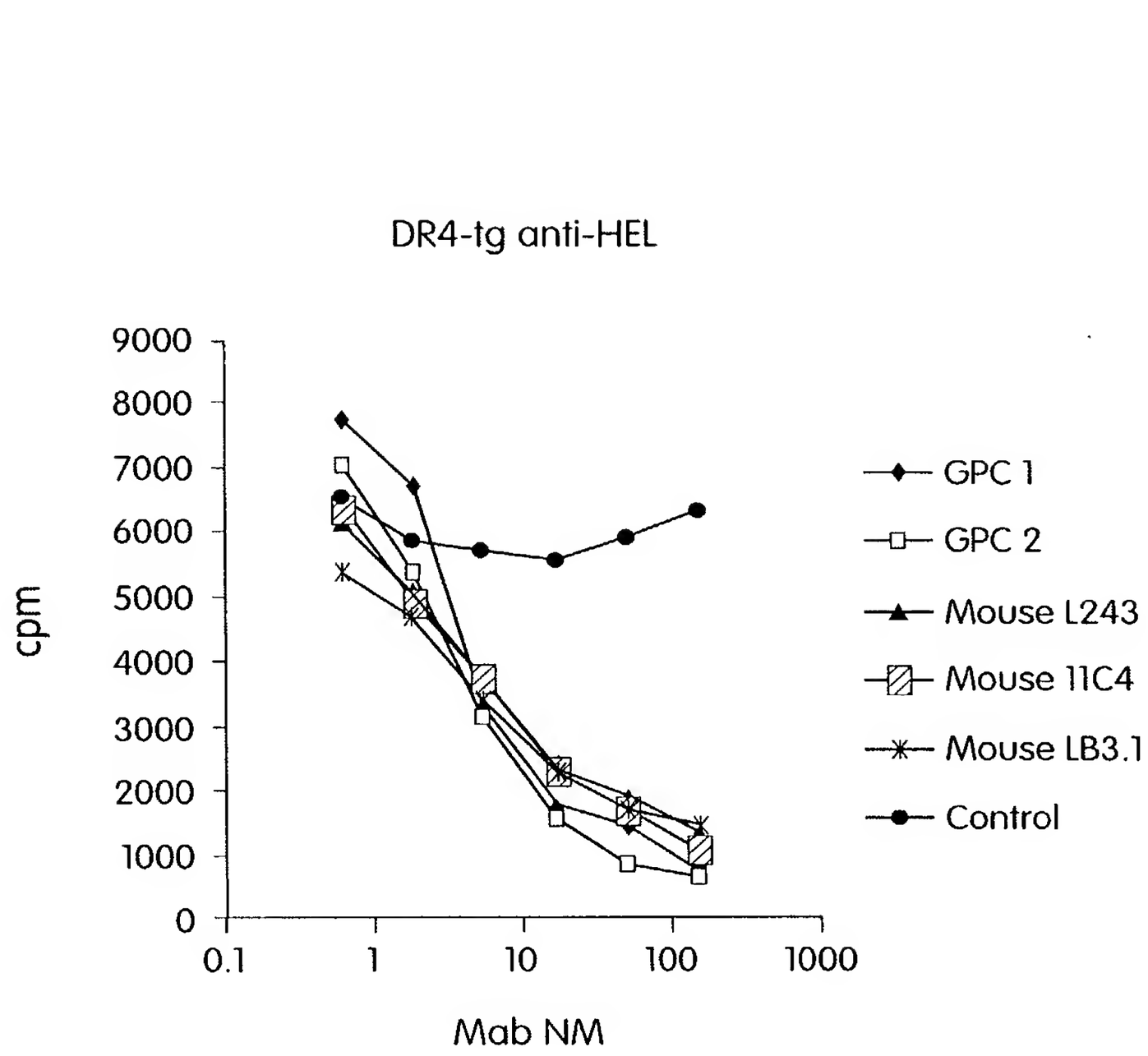
DR4-tg anti-HEL
9000
8000
7000
6000
5000
4000
3000
2000
1000
0
cpm
0.1
1
10
100
1000
Mab NM
GPC 1
GPC 2
Mouse L243
Mouse 11C4
Mouse LB3.1
Control

Fig. 9E

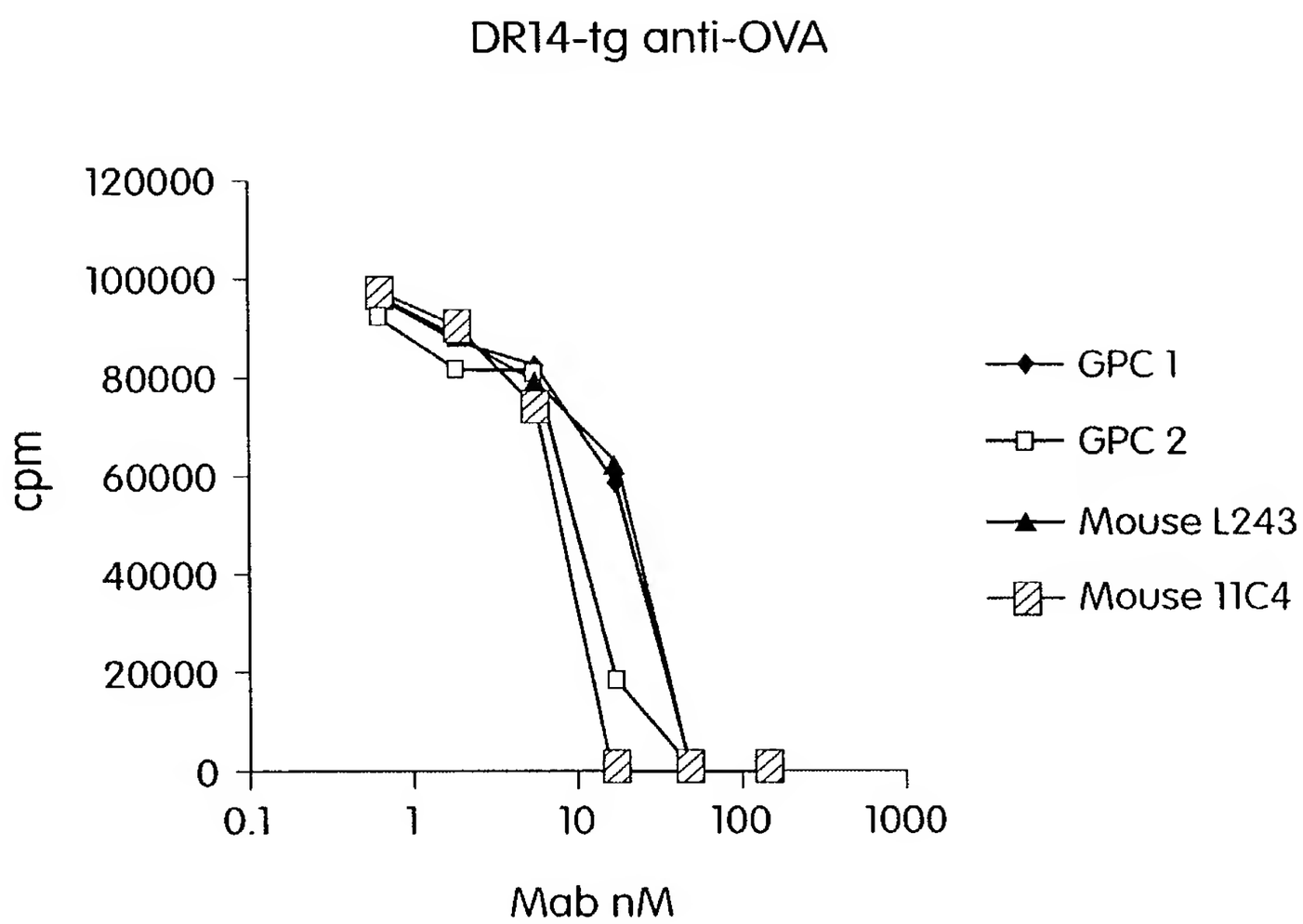
DR14-tg anti-OVA
120000
100000
80000
60000
40000
20000
0
cpm
0.1
1
10
100
1000
Mab nM
GPC 1
GPC 2
Mouse L243
Mouse 11C4

Fig. 9F

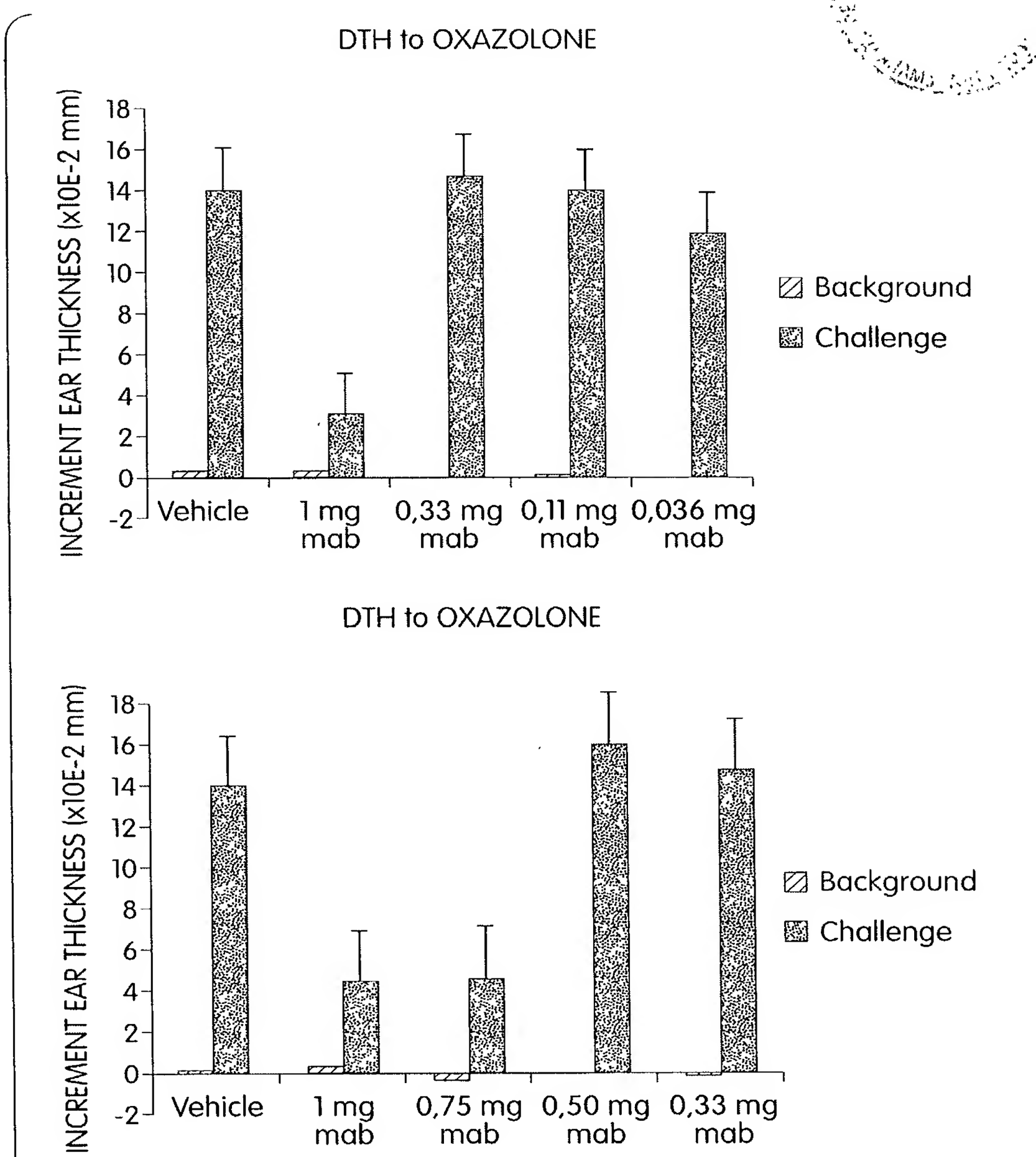
DTH to OXAZOLONE
INCREMENT EAR THICKNESS (x10E-2 mm)
18
16
14
12
10
8
6
4
2
0
-2
Vehicle
1 mg mab
0,33 mg mab
0,11 mg mab
0,036 mg mab
Background
Challenge
DTH to OXAZOLONE
INCREMENT EAR THICKNESS (x10E-2 mm)
18
16
14
12
10
8
6
4
2
0
-2
Vehicle
1 mg mab
0,75 mg mab
0,50 mg mab
0,33 mg mab
Background
Challenge

Fig. 9G

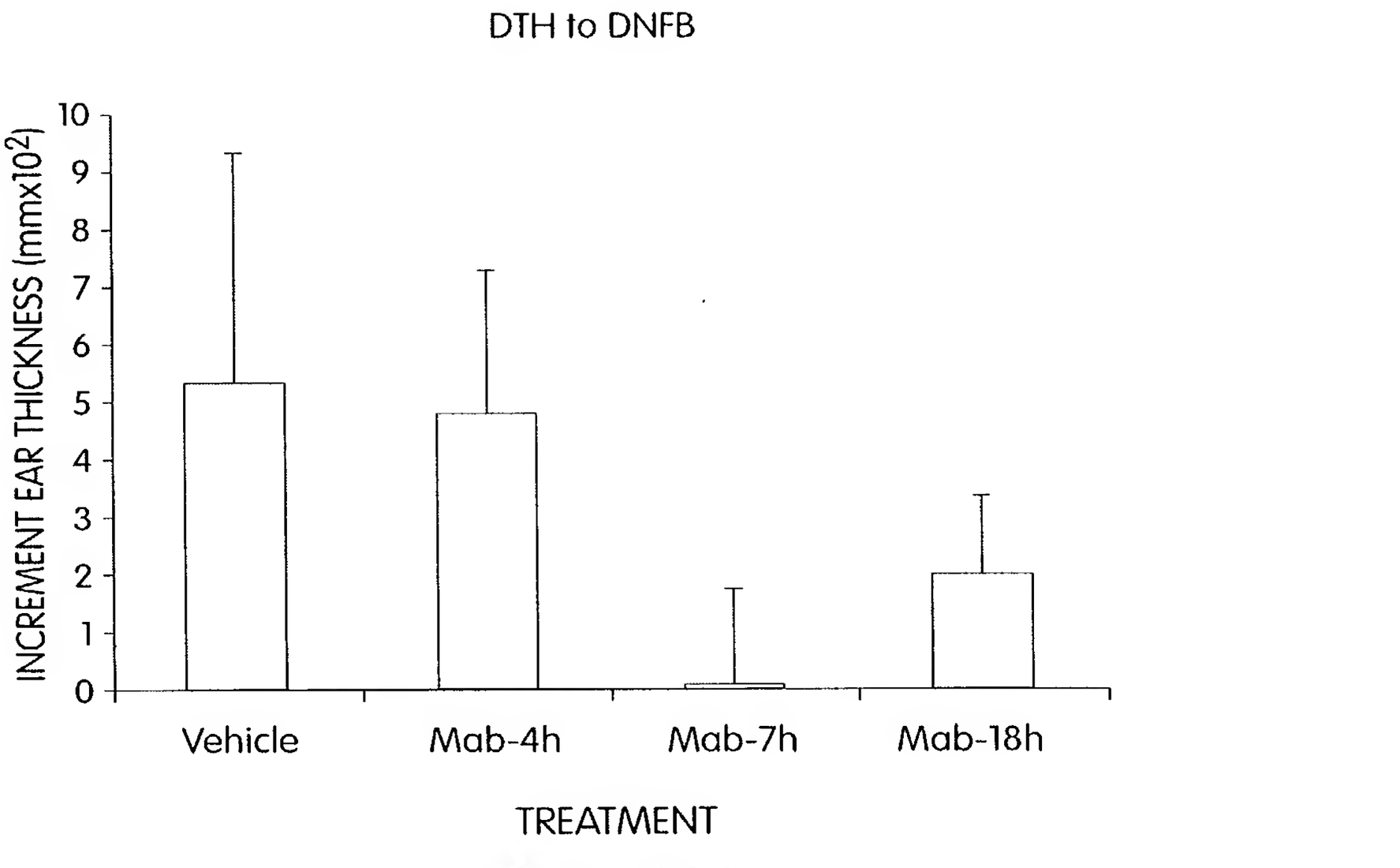
DTH to DNFB
INCREMENT EAR THICKNESS (mmx10²)
10
9
8
7
6
5
4
3
2
1
0
Vehicle
Mab-4h
Mab-7h
Mab-18h
TREATMENT

Fig. 9H

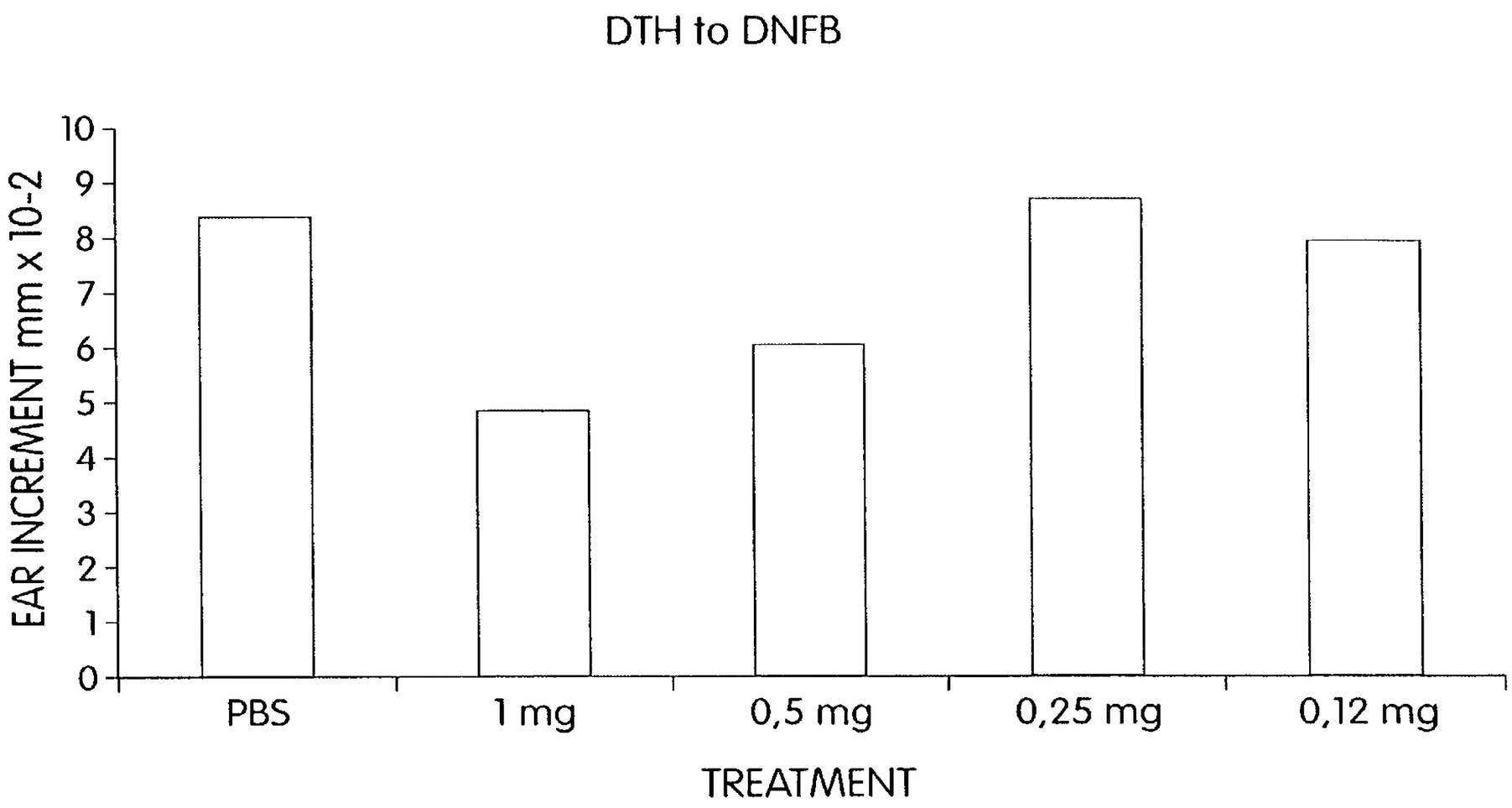
DTH to DNFB
EAR INCREMENT mm x 10-2
0
1
2
3
4
5
6
7
8
9
10
PBS
1 mg
0,5 mg
0,25 mg
0,12 mg
TREATMENT

Fig. 9l

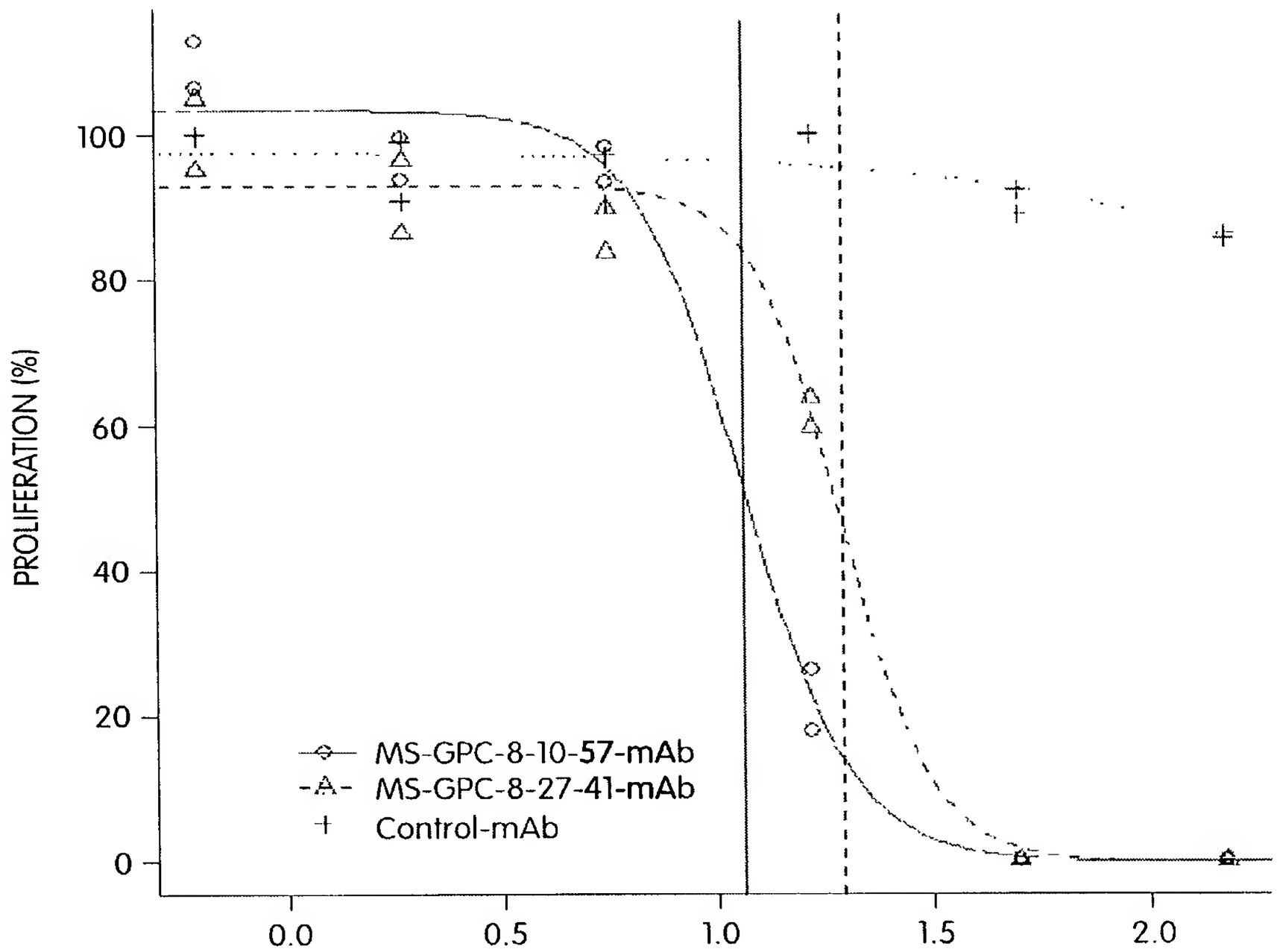
PROLIFERATION (%)
100
80
60
40
20
0
0.0
0.5
1.0
1.5
2.0
MS-GPC-8-10-57-mAb
MS-GPC-8-27-41-mAb
Control-mAb
Log10(mAb concentration/nM)

Fig. 10

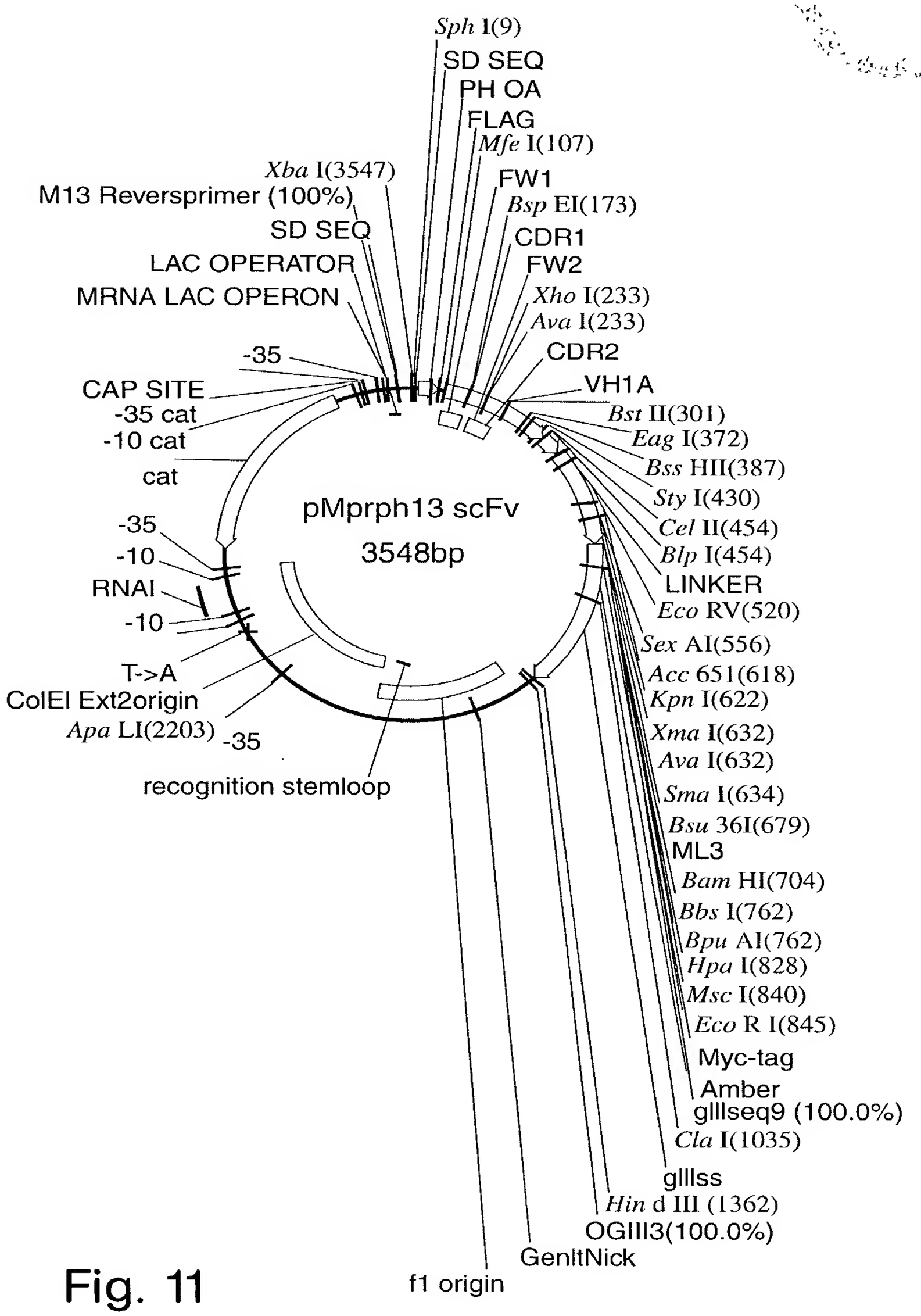
pMprph13 scFv
3548bp
Sph I(9)
SD SEQ
PH OA
FLAG
Mfe I(107)
FW1
Bsp EI(173)
CDR1
FW2
Xho I(233)
Ava I(233)
CDR2
VH1A
Bst II(301)
Eag I(372)
Bss HII(387)
Sty I(430)
Cel II(454)
Blp I(454)
LINKER
Eco RV(520)
Sex AI(556)
Acc 651(618)
Kpn I(622)
Xma I(632)
Ava I(632)
Sma I(634)
Bsu 36I(679)
ML3
Bam HI(704)
Bbs I(762)
Bpu AI(762)
Hpa I(828)
Msc I(840)
Eco R I(845)
Myc-tag
Amber
gIIIseq9 (100.0%)
Cla I(1035)
gIIIss
Hin d III (1362)
OGIII3(100.0%)
GenItNick
f1 origin
Xba I(3547)
M13 Reversprimer (100%)
SD SEQ
LAC OPERATOR
MRNA LAC OPERON
-35
CAP SITE
-35 cat
-10 cat
cat
-35
-10
RNAI
-10
T->A
ColEI Ext2origin
Apa LI(2203)
-35
recognition stemloop

Fig. 11

```
      XbaISphI
      ~~~~~~~~~~
  1   AGAGCATGCG TAGGAGAAAA TAAAATGAAA CAAAGCACTA TTGCACTGGC
      TCTCGTACGC ATCCTCTTTT ATTTTACTTT GTTTCGTGAT AACGTGACCG

 51   ACTCTTACCG TTGCTCTTCA CCCCTGTTAC CAAAGCCGAC TACAAAGATG
      TGAGAATGGC AACGAGAAGT GGGGACAATG GTTTCGGCTG ATGTTTCTAC

            MfeI
           ~~~~~~~
101   AAGTGCAATT GGTTCAGTCT GGCGCGGAAG TGAAAAAACC GGGCAGCAGC
      TTCACGTTAA CCAAGTCAGA CCGCGCCTTC ACTTTTTTGG CCCGTCGTCG

                                  BspEI
                                 ~~~~~~
151   GTGAAAGTGA GCTGCAAAGC CTCCGGAGGC ACTTTTAGCA GCTATGCGAT
      CACTTTCACT CGACGTTTCG GAGGCCTCCG TGAAAATCGT CGATACGCTA

                                           XhoI
                                          ~~~~~~
                                           AvaI
                                          ~~~~~~
201   TAGCTGGGTG CGCCAAGCCC CTGGGCAGGG TCTCGAGTGG ATGGGCGGCA
      ATCGACCCAC GCGGTTCGGG GACCCGTCCC AGAGCTCACC TACCCGCCGT

                                                      BstEII
                                                      ~
251   TTATTCCGAT TTTTGGCACG GCGAACTACG CGCAGAAGTT TCAGGGCCGG
      AATAAGGCTA AAAACCGTGC CGCTTGATGC GCGTCTTCAA AGTCCCGGCC

      BstEII
      ~~~~~~
301   GTGACCATTA CCGCGGATGA AAGCACCAGC ACCGCGTATA TGGAACTGAG
      CACTGGTAAT GGCGCCTACT TTCGTGGTCG TGGCGCATAT ACCTTGACTC

                                  EagI            BssHII
                                 ~~~~~~          ~~~~~~~
351   CAGCCTGCGT AGCGAAGATA CGGCCGTGTA TTATTGCGCG CGTTATTATG
      GTCGGACGCA TCGCTTCTAT GCCGGCACAT AATAACGCGC GCAATAATAC

                                                 StyI
                                                ~~~~~~~
401   ATCGTATGTA TAATATGGAT TATTGGGGCC AAGGCACCCT GGTGACGGTT
      TAGCATACAT ATTATACCTA ATAACCCCGG TTCCGTGGGA CCACTGCCAA

        BlpI
       ~~~~~~~
        CelII
       ~~~~~~~
451   AGCTCAGCGG GTGGCGGTTC TGGCGGCGGT GGGAGCGGTG GCGGTGGTTC
```

Fig. 11 (cont.)

```
      TCGAGTCGCC CACCGCCAAG ACCGCCGCCA CCCTCGCCAC CGCCACCAAG

                           EcoRV
                          ~~~~~~~~
501   TGGCGGTGGT GGTTCCGATA TCGAACTGAC CCAGCCGCCT TCAGTGAGCG
      ACCGCCACCA CCAAGGCTAT AGCTTGACTG GGTCGGCGGA AGTCACTCGC

            SexAI
           ~~~~~~~~~
551   TTGCACCAGG TCAGACCGCG CGTATCTCGT GTAGCGGCGA TGCGCTGGGC
      AACGTGGTCC AGTCTGGCGC GCATAGAGCA CATCGCCGCT ACGCGACCCG

                                                 XmaI
                                                ~~~~~~~
                              KpnI               SmaI
                             ~~~~~~~            ~~~~~~
                             Acc65I              AvaI
                             ~~~~~~~            ~~~~~~
601   GATAAATACG CGAGCTGGTA CCAGCAGAAA CCCGGGCAGG CGCCAGTTCT
      CTATTTATGC GCTCGACCAT GGTCGTCTTT GGGCCCGTCC GCGGTCAAGA

                                       Bsu36I
                                      ~~~~~~~~
651   GGTGATTTAT GATGATTCTG ACCGTCCCTC AGGCATCCCG GAACGCTTTA
      CCACTAAATA CTACTAAGAC TGGCAGGGAG TCCGTAGGGC CTTGCGAAAT

         BamHI
        ~~~~~~
701   GCGGATCCAA CAGCGGCAAC ACCGCGACCC TGACCATTAG CGGCACTCAG
      CGCCTAGGTT GTCGCCGTTG TGGCGCTGGG ACTGGTAATC GCCGTGAGTC

          BpuAI
         ~~~~~~
          BbsI
         ~~~~~~
751   GCGGAAGACG AAGCGGATTA TTATTGCCAG AGCTATGACG CTCATATGCG
      CGCCTTCTGC TTCGCCTAAT AATAACGGTC TCGATACTGC GAGTATACGC

                                      HpaI          MscI     EcoRI
                                     ~~~~~~        ~~~~~~~ ~~~~~~
801   TCCTGTGTTT GGCGGCGGCA CGAAGTTAAC CGTTCTTGGC CAGGAATTCG
      AGGACACAAA CCGCCGCCGT GCTTCAATTG GCAAGAACCG GTCCTTAAGC

851   AGCAGAAGCT GATCTCTGAG GAGGATCTGA ACTAGGGTGG TGGCTCTGGT
      TCGTCTTCGA CTAGAGACTC CTCCTAGACT TGATCCCACC ACCGAGACCA

901   TCCGGTGATT TTGATTATGA AAAGATGGCA AACGCTAATA AGGGGGCTAT
      AGGCCACTAA AACTAATACT TTTCTACCGT TTGCGATTAT TCCCCCGATA
                                    gIIIseq9  100.0%
                                   ======================

951   GACCGAAAAT GCCGATGAAA ACGCGCTACA GTCTGACGCT AAAGGCAAAC
```

Fig. 11 (cont.)

```
          CTGGCTTTTA CGGCTACTTT TGCGCGATGT CAGACTGCGA TTTCCGTTTG

                                                 ClaI
                                                 ~~~~~~
1001      TTGATTCTGT CGCTACTGAT TACGGTGCTG CTATCGATGG TTTCATTGGT
          AACTAAGACA GCGATGACTA ATGCCACGAC GATAGCTACC AAAGTAACCA

1051      GACGTTTCCG GCCTTGCTAA TGGTAATGGT GCTACTGGTG ATTTTGCTGG
          CTGCAAAGGC CGGAACGATT ACCATTACCA CGATGACCAC TAAAACGACC

1101      CTCTAATTCC CAAATGGCTC AAGTCGGTGA CGGTGATAAT TCACCTTTAA
          GAGATTAAGG GTTTACCGAG TTCAGCCACT GCCACTATTA AGTGGAAATT

1151      TGAATAATTT CCGTCAATAT TTACCTTCCC TCCCTCAATC GGTTGAATGT
          ACTTATTAAA GGCAGTTATA AATGGAAGGG AGGGAGTTAG CCAACTTACA

1201      CGCCCTTTTG TCTTTGGCGC TGGTAAACCA TATGAATTTT CTATTGATTG
          GCGGGAAAAC AGAAACCGCG ACCATTTGGT ATACTTAAAA GATAACTAAC

1251      TGACAAAATA AACTTATTCC GTGGTGTCTT TGCGTTTCTT TTATATGTTG
          ACTGTTTTAT TTGAATAAGG CACCACAGAA ACGCAAAGAA AATATACAAC

1301      CCACCTTTAT GTATGTATTT TCTACGTTTG CTAACATACT GCGTAATAAG
          GGTGGAAATA CATACATAAA AGATGCAAAC GATTGTATGA CGCATTATTC

                    HindIII
                    ~~~~~~
1351      GAGTCTTGAT AAGCTTGACC TGTGAAGTGA AAAATGGCGC AGATTGTGCG
          CTCAGAACTA TTCGAACTGG ACACTTCACT TTTTACCGCG TCTAACACGC
                               OGIII3  100.0%
                              ====================

1401      ACATTTTTTT TGTCTGCCGT TTAATGAAAT TGTAAACGTT AATATTTTGT
          TGTAAAAAAA ACAGACGGCA AATTACTTTA ACATTTGCAA TTATAAAACA

1451      TAAAATTCGC GTTAAATTTT TGTTAAATCA GCTCATTTTT TAACCAATAG
          ATTTTAAGCG CAATTTAAAA ACAATTTAGT CGAGTAAAAA ATTGGTTATC

1501      GCCGAAATCG GCAAAATCCC TTATAAATCA AAAGAATAGA CCGAGATAGG
          CGGCTTTAGC CGTTTTAGGG AATATTTAGT TTTCTTATCT GGCTCTATCC

1551      GTTGAGTGTT GTTCCAGTTT GGAACAAGAG TCCACTATTA AAGAACGTGG
          CAACTCACAA CAAGGTCAAA CCTTGTTCTC AGGTGATAAT TTCTTGCACC

1601      ACTCCAACGT CAAAGGGCGA AAAACCGTCT ATCAGGGCGA TGGCCCACTA
          TGAGGTTGCA GTTTCCCGCT TTTTGGCAGA TAGTCCCGCT ACCGGGTGAT

1651      CGAGAACCAT CACCCTAATC AAGTTTTTTG GGGTCGAGGT GCCGTAAAGC
          GCTCTTGGTA GTGGGATTAG TTCAAAAAAC CCCAGCTCCA CGGCATTTCG

1701      ACTAAATCGG AACCCTAAAG GGAGCCCCCG ATTTAGAGCT TGACGGGGAA
          TGATTTAGCC TTGGGATTTC CCTCGGGGGC TAAATCTCGA ACTGCCCCTT
```

Fig. 11 (cont.)

```
1751   AGCCGGCGAA CGTGGCGAGA AAGGAAGGGA AGAAAGCGAA AGGAGCGGGC
       TCGGCCGCTT GCACCGCTCT TTCCTTCCCT TCTTTCGCTT TCCTCGCCCG

1801   GCTAGGGCGC TGGCAAGTGT AGCGGTCACG CTGCGCGTAA CCACCACACC
       CGATCCCGCG ACCGTTCACA TCGCCAGTGC GACGCGCATT GGTGGTGTGG

1851   CGCCGCGCTT AATGCGCCGC TACAGGGCGC GTGCTAGCCA TGTGAGCAAA
       GCGGCGCGAA TTACGCGGCG ATGTCCCGCG CACGATCGGT ACACTCGTTT

1901   AGGCCAGCAA AAGGCCAGGA ACCGTAAAAA GGCCGCGTTG CTGGCGTTTT
       TCCGGTCGTT TTCCGGTCCT TGGCATTTTT CCGGCGCAAC GACCGCAAAA

1951   TCCATAGGCT CCGCCCCCCT GACGAGCATC ACAAAAATCG ACGCTCAAGT
       AGGTATCCGA GGCGGGGGGA CTGCTCGTAG TGTTTTTAGC TGCGAGTTCA

2001   CAGAGGTGGC GAAACCCGAC AGGACTATAA AGATACCAGG CGTTTCCCCC
       GTCTCCACCG CTTTGGGCTG TCCTGATATT TCTATGGTCC GCAAAGGGGG

2051   TGGAAGCTCC CTCGTGCGCT CTCCTGTTCC GACCCTGCCG CTTACCGGAT
       ACCTTCGAGG GAGCACGCGA GAGGACAAGG CTGGGACGGC GAATGGCCTA

2101   ACCTGTCCGC CTTTCTCCCT TCGGGAAGCG TGGCGCTTTC TCATAGCTCA
       TGGACAGGCG GAAAGAGGGA AGCCCTTCGC ACCGCGAAAG AGTATCGAGT

2151   CGCTGTAGGT ATCTCAGTTC GGTGTAGGTC GTTCGCTCCA AGCTGGGCTG
       GCGACATCCA TAGAGTCAAG CCACATCCAG CAAGCGAGGT TCGACCCGAC

         ApaLI
        ~~~~~~
2201   TGTGCACGAA CCCCCCGTTC AGTCCGACCG CTGCGCCTTA TCCGGTAACT
       ACACGTGCTT GGGGGGCAAG TCAGGCTGGC GACGCGGAAT AGGCCATTGA

2251   ATCGTCTTGA GTCCAACCCG GTAAGACACG ACTTATCGCC ACTGGCAGCA
       TAGCAGAACT CAGGTTGGGC CATTCTGTGC TGAATAGCGG TGACCGTCGT

2301   GCCACTGGTA ACAGGATTAG CAGAGCGAGG TATGTAGGCG GTGCTACAGA
       CGGTGACCAT TGTCCTAATC GTCTCGCTCC ATACATCCGC CACGATGTCT

2351   GTTCTTGAAG TGGTGGCCTA ACTACGGCTA CACTAGAAGA ACAGTATTTG
       CAAGAACTTC ACCACCGGAT TGATGCCGAT GTGATCTTCT TGTCATAAAC

2401   GTATCTGCGC TCTGCTGTAG CCAGTTACCT TCGGAAAAAG AGTTGGTAGC
       CATAGACGCG AGACGACATC GGTCAATGGA AGCCTTTTTC TCAACCATCG

2451   TCTTGATCCG GCAAACAAAC CACCGCTGGT AGCGGTGGTT TTTTTGTTTG
       AGAACTAGGC CGTTTGTTTG GTGGCGACCA TCGCCACCAA AAAAACAAAC

2501   CAAGCAGCAG ATTACGCGCA GAAAAAAAGG ATCTCAAGAA GATCCTTTGA
       GTTCGTCGTC TAATGCGCGT CTTTTTTTCC TAGAGTTCTT CTAGGAAACT

2551   TCTTTTCTAC GGGGTCTGAC GCTCAGTGGA ACGAAAACTC ACGTTAAGGG
```

Fig. 11 (cont.)

```
        AGAAAAGATG CCCCAGACTG CGAGTCACCT TGCTTTTGAG TGCAATTCCC

2601    ATTTTGGTCA GATCTAGCAC CAGGCGTTTA AGGGCACCAA TAACTGCCTT
        TAAAACCAGT CTAGATCGTG GTCCGCAAAT TCCCGTGGTT ATTGACGGAA

2651    AAAAAAATTA CGCCCCGCCC TGCCACTCAT CGCAGTACTG TTGTAATTCA
        TTTTTTTAAT GCGGGGCGGG ACGGTGAGTA GCGTCATGAC AACATTAAGT

2701    TTAAGCATTC TGCCGACATG GAAGCCATCA CAAACGGCAT GATGAACCTG
        AATTCGTAAG ACGGCTGTAC CTTCGGTAGT GTTTGCCGTA CTACTTGGAC

2751    AATCGCCAGC GGCATCAGCA CCTTGTCGCC TTGCGTATAA TATTTGCCCA
        TTAGCGGTCG CCGTAGTCGT GGAACAGCGG AACGCATATT ATAAACGGGT

2801    TAGTGAAAAC GGGGGCGAAG AAGTTGTCCA TATTGGCTAC GTTTAAATCA
        ATCACTTTTG CCCCCGCTTC TTCAACAGGT ATAACCGATG CAAATTTAGT

2851    AAACTGGTGA AACTCACCCA GGGATTGGCT GAGACGAAAA ACATATTCTC
        TTTGACCACT TTGAGTGGGT CCCTAACCGA CTCTGCTTTT TGTATAAGAG

2901    AATAAACCCT TTAGGGAAAT AGGCCAGGTT TTCACCGTAA CACGCCACAT
        TTATTTGGGA AATCCCTTTA TCCGGTCCAA AAGTGGCATT GTGCGGTGTA

2951    CTTGCGAATA TATGTGTAGA AACTGCCGGA AATCGTCGTG GTATTCACTC
        GAACGCTTAT ATACACATCT TTGACGGCCT TTAGCAGCAC CATAAGTGAG

3001    CAGAGCGATG AAAACGTTTC AGTTTGCTCA TGGAAAACGG TGTAACAAGG
        GTCTCGCTAC TTTTGCAAAG TCAAACGAGT ACCTTTTGCC ACATTGTTCC

3051    GTGAACACTA TCCCATATCA CCAGCTCACC GTCTTTCATT GCCATACGGA
        CACTTGTGAT AGGGTATAGT GGTCGAGTGG CAGAAAGTAA CGGTATGCCT

3101    ACTCCGGGTG AGCATTCATC AGGCGGGCAA GAATGTGAAT AAAGGCCGGA
        TGAGGCCCAC TCGTAAGTAG TCCGCCCGTT CTTACACTTA TTTCCGGCCT

3151    TAAAACTTGT GCTTATTTTT CTTTACGGTC TTTAAAAAGG CCGTAATATC
        ATTTTGAACA CGAATAAAAA GAAATGCCAG AAATTTTTCC GGCATTATAG

3201    CAGCTGAACG GTCTGGTTAT AGGTACATTG AGCAACTGAC TGAAATGCCT
        GTCGACTTGC CAGACCAATA TCCATGTAAC TCGTTGACTG ACTTTACGGA

3251    CAAAATGTTC TTTACGATGC CATTGGGATA TATCAACGGT GGTATATCCA
        GTTTTACAAG AAATGCTACG GTAACCCTAT ATAGTTGCCA CCATATAGGT

3301    GTGATTTTTT TCTCCATTTT AGCTTCCTTA GCTCCTGAAA ATCTCGATAA
        CACTAAAAAA AGAGGTAAAA TCGAAGGAAT CGAGGACTTT TAGAGCTATT

3351    CTCAAAAAAT ACGCCCGGTA GTGATCTTAT TTCATTATGG TGAAAGTTGG
        GAGTTTTTTA TGCGGGCCAT CACTAGAATA AAGTAATACC ACTTTCAACC

3401    AACCTCACCC GACGTCTAAT GTGAGTTAGC TCACTCATTA GGCACCCCAG
        TTGGAGTGGG CTGCAGATTA CACTCAATCG AGTGAGTAAT CCGTGGGGTC
```

Fig. 11 (cont.)

```
3451   GCTTTACACT TTATGCTTCC GGCTCGTATG TTGTGTGGAA TTGTGAGCGG
       CGAAATGTGA AATACGAAGG CCGAGCATAC AACACACCTT AACACTCGCC

                   M13 Reverse  primer 100.0%          XbaI
                       ====================           ~~
3501   ATAACAATTT CACACAGGAA ACAGCTATGA CCATGATTAC GAATTTCT
       TATTGTTAAA GTGTGTCCTT TGTCGATACT GGTACTAATG CTTAAAGA
```

Fig. 11 (cont.)

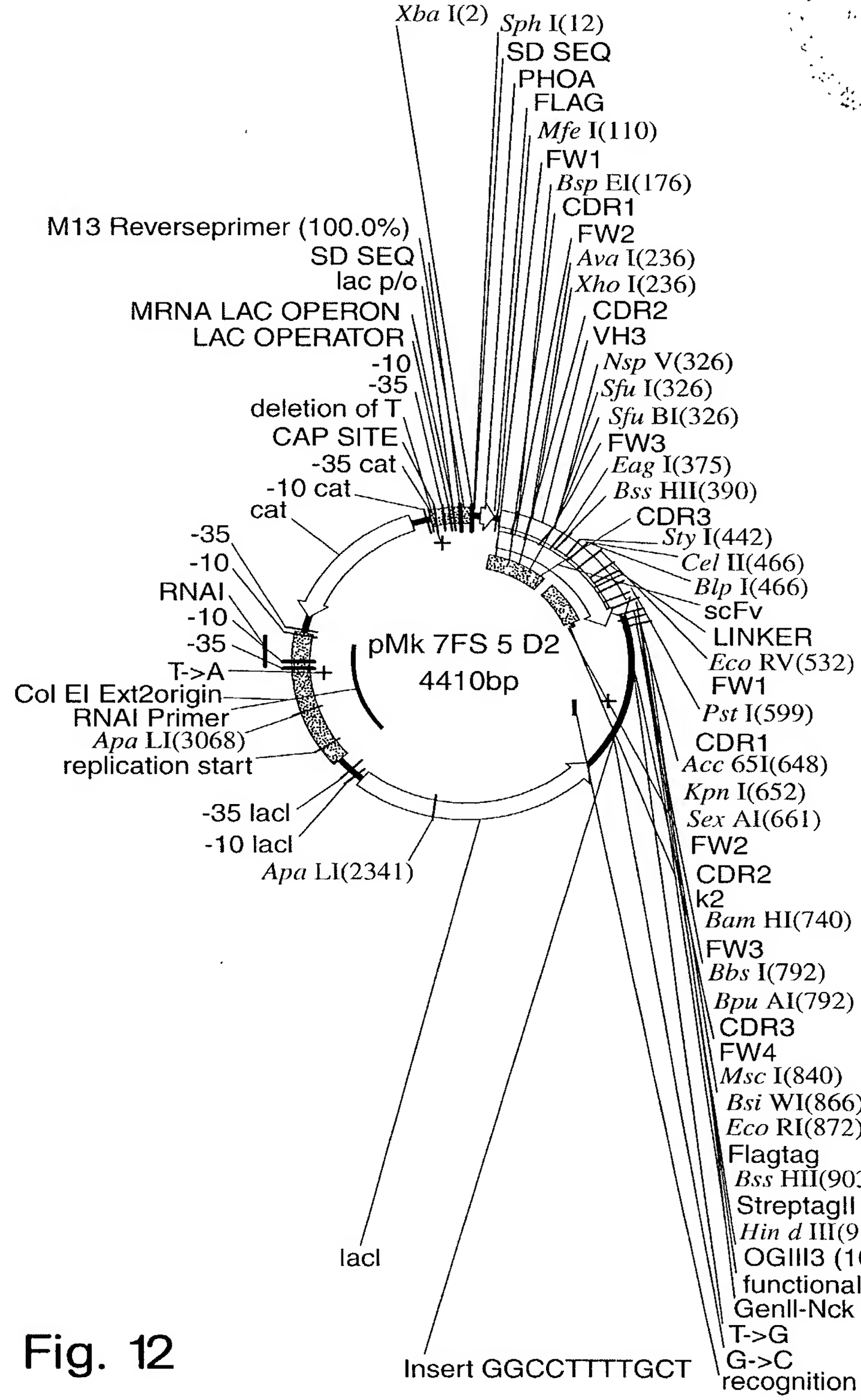
Xba I(2)
Sph I(12)
SD SEQ
PHOA
FLAG
Mfe I(110)
FW1
Bsp EI(176)
CDR1
FW2
Ava I(236)
Xho I(236)
CDR2
VH3
Nsp V(326)
Sfu I(326)
Sfu BI(326)
FW3
Eag I(375)
Bss HII(390)
CDR3
Sty I(442)
Cel II(466)
Blp I(466)
scFv
LINKER
Eco RV(532)
FW1
Pst I(599)
CDR1
Acc 65I(648)
Kpn I(652)
Sex AI(661)
FW2
CDR2
k2
Bam HI(740)
FW3
Bbs I(792)
Bpu AI(792)
CDR3
FW4
Msc I(840)
Bsi WI(866)
Eco RI(872)
Flagtag
Bss HII(903)
StreptagII
Hin d III(939)
OGIII3 (100%)
functional ss ori
GenII-Nck
T->G
G->C
recognition stem loop
M13 Reverseprimer (100.0%)
SD SEQ
lac p/o
MRNA LAC OPERON
LAC OPERATOR
-10
-35
deletion of T
CAP SITE
-35 cat
-10 cat
cat
-35
-10
RNAI
-10
-35
T->A
Col EI Ext2origin
RNAI Primer
Apa LI(3068)
replication start
-35 lacI
-10 lacI
Apa LI(2341)
pMk 7FS 5 D2
4410bp
lacI
Insert GGCCTTTTGCT

Fig. 12

```
      XbaI  SphI
      ~~~~~~~~~~~~~
  1   TCTAGAGCAT GCGTAGGAGA AAATAAAATG AAACAAAGCA CTATTGCACT
      AGATCTCGTA CGCATCCTCT TTTATTTTAC TTTGTTTCGT GATAACGTGA

 51   GGCACTCTTA CCGTTGCTCT TCACCCCTGT TACCAAAGCC GACTACAAAG
      CCGTGAGAAT GGCAACGAGA AGTGGGGACA ATGGTTTCGG CTGATGTTTC

                MfeI
               ~~~~~~~
101   ATGAAGTGCA ATTGGTGGAA AGCGGCGGCG GCCTGGTGCA ACCGGGCGGC
      TACTTCACGT TAACCACCTT TCGCCGCCGC CGGACCACGT TGGCCCGCCG

                                    BspEI
                                   ~~~~~~
151   AGCCTGCGTC TGAGCTGCGC GGCCTCCGGA TTTACCTTTA GCAGCTATGC
      TCGGACGCAG ACTCGACGCG CCGGAGGCCT AAATGGAAAT CGTCGATACG

                                          XhoI
                                         ~~~~~~
                                          AvaI
                                         ~~~~~~
201   GATGAGCTGG GTGCGCCAAG CCCCTGGGAA GGGTCTCGAG TGGGTGAGCG
      CTACTCGACC CACGCGGTTC GGGGACCCTT CCCAGAGCTC ACCCACTCGC

251   CGATTAGCGG TAGCGGCGGC AGCACCTATT ATGCGGATAG CGTGAAAGGC
      GCTAATCGCC ATCGCCGCCG TCGTGGATAA TACGCCTATC GCACTTTCCG

                                   BstBI
                                  ~~~~~~
                                   SfuI
                                  ~~~~~~
                                   NspV
                                  ~~~~~~
301   CGTTTTACCA TTTCACGTGA TAATTCGAAA AACACCCTGT ATCTGCAAAT
      GCAAAATGGT AAAGTGCACT ATTAAGCTTT TTGTGGGACA TAGACGTTTA

                                   EagI              BssHII
                                  ~~~~~~            ~~~~~~~
351   GAACAGCCTG CGTGCGGAAG ATACGGCCGT GTATTATTGC GCGCGTGTTA
      CTTGTCGGAC GCACGCCTTC TATGCCGGCA CATAATAACG CGCGCACAAT

                                                      StyI
                                                     ~~~~~~
401   AGAAGCATTT TTCTCGTAAG AATTGGTTTG ATTATTGGGG CCAAGGCACC
      TCTTCGTAAA AAGAGCATTC TTAACCAAAC TAATAACCCC GGTTCCGTGG
```

Fig. 12 (cont.)

```
                          BlpI
                          ~~~~~~~
                          CelII
                          ~~~~~~~
451   CTGGTGACGG TTAGCTCAGC GGGTGGCGGT TCTGGCGGCG GTGGGAGCGG
      GACCACTGCC AATCGAGTCG CCCACCGCCA AGACCGCCGC CACCCTCGCC

                                              EcoRV
                                              ~~~~~~~
501   TGGCGGTGGT TCTGGCGGTG GTGGTTCCGA TATCGTGATG ACCCAGAGCC
      ACCGCCACCA AGACCGCCAC CACCAAGGCT ATAGCACTAC TGGGTCTCGG

                                                    PstI
                                                    ~~~~~~
551   CACTGAGCCT GCCAGTGACT CCGGGCGAGC CTGCGAGCAT TAGCTGCAGA
      GTGACTCGGA CGGTCACTGA GGCCCGCTCG GACGCTCGTA ATCGACGTCT

                                                   KpnI
                                                   ~~~~
                                                 Acc65I
                                                 ~~~~
601   AGCAGCCAAA GCCTGCTGCA TAGCAACGGC TATAACTATC TGGATTGGTA
      TCGTCGGTTT CGGACGACGT ATCGTTGCCG ATATTGATAG ACCTAACCAT

      KpnI
      ~~
      Acc65I      SexAI
      ~~        ~~~~~~~~
651   CCTTCAAAAA CCAGGTCAAA GCCCGCAGCT ATTAATTTAT CTGGGCAGCA
      GGAAGTTTTT GGTCCAGTTT CGGGCGTCGA TAATTAAATA GACCCGTCGT

                                                  BamHI
                                                  ~~~~~~~
701   ACCGTGCCAG TGGGGTCCCG GATCGTTTTA GCGGCTCTGG ATCCGGCACC
      TGGCACGGTC ACCCCAGGGC CTAGCAAAAT CGCCGAGACC TAGGCCGTGG

                                                BpuAI
                                                ~~~~~~
                                                BbsI
                                                ~~~~~~
751   GATTTTACCC TGAAAATTAG CCGTGTGGAA GCTGAAGACG TGGGCGTGTA
      CTAAAATGGG ACTTTTAATC GGCACACCTT CGACTTCTGC ACCCGCACAT

                                                 MscI
                                                 ~~~~~~~
801   TTATTGCCAG CAGCATTATA CCACCCCGCC GACCTTTGGC CAGGGTACGA
      AATAACGGTC GTCGTAATAT GGTGGGGCGG CTGGAAACCG GTCCCATGCT
```

Fig. 12 (cont.)

```
                          BsiWI   EcoRI
                          ~~~~~~~~~~~~~~
851   AAGTTGAAAT TAAACGTACG GAATTCGACT ATAAAGATGA CGATGACAAA
      TTCAACTTTA ATTTGCATGC CTTAAGCTGA TATTTCTACT GCTACTGTTT

       BssHII                                          HindIII
       ~~~~~~                                          ~~~~~~~
901   GGCGCGCCGT GGAGCCACCC GCAGTTTGAA AAATGATAAG CTTGACCTGT
      CCGCGCGGCA CCTCGGTGGG CGTCAAACTT TTTACTATTC GAACTGGACA
                                                   OGIII3  100.0%
                                                   =======

 951  GAAGTGAAAA ATGGCGCAGA TTGTGCGACA TTTTTTTTGT CTGCCGTTTA
      CTTCACTTTT TACCGCGTCT AACACGCTGT AAAAAAAACA GACGGCAAAT
      OGIII3 100.0%
      ============

1001  ATTAAAGGGG GGGGGGGGCC GGCCTGGGGG GGGGTGTACA TGAAATTGTA
      TAATTTCCCC CCCCCCCCGG CCGGACCCCC CCCCACATGT ACTTTAACAT

1051  AACGTTAATA TTTTGTTAAA ATTCGCGTTA AATTTTTGTT AAATCAGCTC
      TTGCAATTAT AAAACAATTT TAAGCGCAAT TTAAAAACAA TTTAGTCGAG

1101  ATTTTTTAAC CAATAGGCCG AAATCGGCAA AATCCCTTAT AAATCAAAAG
      TAAAAAATTG GTTATCCGGC TTTAGCCGTT TTAGGGAATA TTTAGTTTTC

1151  AATAGACCGA GATAGGGTTG AGTGTTGTTC CAGTTTGGAA CAAGAGTCCA
      TTATCTGGCT CTATCCCAAC TCACAACAAG GTCAAACCTT GTTCTCAGGT

1201  CTATTAAAGA ACGTGGACTC CAACGTCAAA GGGCGAAAAA CCGTCTATCA
      GATAATTTCT TGCACCTGAG GTTGCAGTTT CCCGCTTTTT GGCAGATAGT

1251  GGGCGATGGC CCACTACGAG AACCATCACC CTAATCAAGT TTTTTGGGGT
      CCCGCTACCG GGTGATGCTC TTGGTAGTGG GATTAGTTCA AAAAACCCCA

1301  CGAGGTGCCG TAAAGCACTA AATCGGAACC CTAAAGGGAG CCCCCGATTT
      GCTCCACGGC ATTTCGTGAT TTAGCCTTGG GATTTCCCTC GGGGGCTAAA

1351  AGAGCTTGAC GGGGAAAGCC GGCGAACGTG GCGAGAAAGG AAGGGAAGAA
      TCTCGAACTG CCCCTTTCGG CCGCTTGCAC CGCTCTTTCC TTCCCTTCTT

1401  AGCGAAAGGA GCGGGCGCTA GGGCGCTGGC AAGTGTAGCG GTCACGCTGC
      TCGCTTTCCT CGCCCGCGAT CCCGCGACCG TTCACATCGC CAGTGCGACG

1451  GCGTAACCAC CACACCCGCC GCGCTTAATG CGCCGCTACA GGGCGCGTGC
      CGCATTGGTG GTGTGGGCGG CGCGAATTAC GCGGCGATGT CCCGCGCACG
```

Fig. 12 (cont.)

```
1501  TAGACTAGTG TTTAAACCGG ACCGGGGGGG GGCTTAAGTG GGCTGCAAAA
      ATCTGATCAC AAATTTGGCC TGGCCCCCCC CCGAATTCAC CCGACGTTTT

1551  CAAAACGGCC TCCTGTCAGG AAGCCGCTTT TATCGGGTAG CCTCACTGCC
      GTTTTGCCGG AGGACAGTCC TTCGGCGAAA ATAGCCCATC GGAGTGACGG

1601  CGCTTTCCAG TCGGGAAACC TGTCGTGCCA GCTGCATCAG TGAATCGGCC
      GCGAAAGGTC AGCCCTTTGG ACAGCACGGT CGACGTAGTC ACTTAGCCGG

1651  AACGCGCGGG GAGAGGCGGT TTGCGTATTG GGAGCCAGGG TGGTTTTTCT
      TTGCGCGCCC CTCTCCGCCA AACGCATAAC CCTCGGTCCC ACCAAAAAGA

1701  TTTCACCAGT GAGACGGGCA ACAGCTGATT GCCCTTCACC GCCTGGCCCT
      AAAGTGGTCA CTCTGCCCGT TGTCGACTAA CGGGAAGTGG CGGACCGGGA

1751  GAGAGAGTTG CAGCAAGCGG TCCACGCTGG TTTGCCCCAG CAGGCGAAAA
      CTCTCTCAAC GTCGTTCGCC AGGTGCGACC AAACGGGGTC GTCCGCTTTT

1801  TCCTGTTTGA TGGTGGTCAG CGGCGGGATA TAACATGAGC TGTCCTCGGT
      AGGACAAACT ACCACCAGTC GCCGCCCTAT ATTGTACTCG ACAGGAGCCA

1851  ATCGTCGTAT CCCACTACCG AGATGTCCGC ACCAACGCGC AGCCCGGACT
      TAGCAGCATA GGGTGATGGC TCTACAGGCG TGGTTGCGCG TCGGGCCTGA

1901  CGGTAATGGC ACGCATTGCG CCCAGCGCCA TCTGATCGTT GGCAACCAGC
      GCCATTACCG TGCGTAACGC GGGTCGCGGT AGACTAGCAA CCGTTGGTCG

1951  ATCGCAGTGG GAACGATGCC CTCATTCAGC ATTTGCATGG TTTGTTGAAA
      TAGCGTCACC CTTGCTACGG GAGTAAGTCG TAAACGTACC AAACAACTTT

2001  ACCGGACATG GCACTCCAGT CGCCTTCCCG TTCCGCTATC GGCTGAATTT
      TGGCCTGTAC CGTGAGGTCA GCGGAAGGGC AAGGCGATAG CCGACTTAAA

2051  GATTGCGAGT GAGATATTTA TGCCAGCCAG CCAGACGCAG ACGCGCCGAG
      CTAACGCTCA CTCTATAAAT ACGGTCGGTC GGTCTGCGTC TGCGCGGCTC

2101  ACAGAACTTA ATGGGCCAGC TAACAGCGCG ATTTGCTGGT GGCCCAATGC
      TGTCTTGAAT TACCCGGTCG ATTGTCGCGC TAAACGACCA CCGGGTTACG

2151  GACCAGATGC TCCACGCCCA GTCGCGTACC GTCCTCATGG GAGAAAATAA
      CTGGTCTACG AGGTGCGGGT CAGCGCATGG CAGGAGTACC CTCTTTTATT

2201  TACTGTTGAT GGGTGTCTGG TCAGAGACAT CAAGAAATAA CGCCGGAACA
      ATGACAACTA CCCACAGACC AGTCTCTGTA GTTCTTTATT GCGGCCTTGT

2251  TTAGTGCAGG CAGCTTCCAC AGCAATAGCA TCCTGGTCAT CCAGCGGATA
      AATCACGTCC GTCGAAGGTG TCGTTATCGT AGGACCAGTA GGTCGCCTAT

                                                    ApaLI
                                                   ~~~~~~~
```

Fig. 12 (cont.)

```
2301   GTTAATAATC AGCCCACTGA CACGTTGCGC GAGAAGATTG TGCACCGCCG
       CAATTATTAG TCGGGTGACT GTGCAACGCG CTCTTCTAAC ACGTGGCGGC

2351   CTTTACAGGC TTCGACGCCG CTTCGTTCTA CCATCGACAC GACCACGCTG
       GAAATGTCCG AAGCTGCGGC GAAGCAAGAT GGTAGCTGTG CTGGTGCGAC

2401   GCACCCAGTT GATCGGCGCG AGATTTAATC GCCGCGACAA TTTGCGACGG
       CGTGGGTCAA CTAGCCGCGC TCTAAATTAG CGGCGCTGTT AAACGCTGCC

2451   CGCGTGCAGG GCCAGACTGG AGGTGGCAAC GCCAATCAGC AACGACTGTT
       GCGCACGTCC CGGTCTGACC TCCACCGTTG CGGTTAGTCG TTGCTGACAA

2501   TGCCCGCCAG TTGTTGTGCC ACGCGGTTAG GAATGTAATT CAGCTCCGCC
       ACGGGCGGTC AACAACACGG TGCGCCAATC CTTACATTAA GTCGAGGCGG

2551   ATCGCCGCTT CCACTTTTTC CCGCGTTTTC GCAGAAACGT GGCTGGCCTG
       TAGCGGCGAA GGTGAAAAAG GGCGCAAAAG CGTCTTTGCA CCGACCGGAC

2601   GTTCACCACG CGGGAAACGG TCTGATAAGA GACACCGGCA TACTCTGCGA
       CAAGTGGTGC GCCCTTTGCC AGACTATTCT CTGTGGCCGT ATGAGACGCT

2651   CATCGTATAA CGTTACTGGT TTCACATTCA CCACCCTGAA TTGACTCTCT
       GTAGCATATT GCAATGACCA AAGTGTAAGT GGTGGGACTT AACTGAGAGA

2701   TCCGGGCGCT ATCATGCCAT ACCGCGAAAG GTTTTGCGCC ATTCGATGCT
       AGGCCCGCGA TAGTACGGTA TGGCGCTTTC CAAAACGCGG TAAGCTACGA

2751   AGCCATGTGA GCAAAAGGCC AGCAAAAGGC CAGGAACCGT AAAAAGGCCG
       TCGGTACACT CGTTTTCCGG TCGTTTTCCG GTCCTTGGCA TTTTTCCGGC

2801   CGTTGCTGGC GTTTTTCCAT AGGCTCCGCC CCCCTGACGA GCATCACAAA
       GCAACGACCG CAAAAAGGTA TCCGAGGCGG GGGGACTGCT CGTAGTGTTT

2851   AATCGACGCT CAAGTCAGAG GTGGCGAAAC CCGACAGGAC TATAAAGATA
       TTAGCTGCGA GTTCAGTCTC CACCGCTTTG GGCTGTCCTG ATATTTCTAT

2901   CCAGGCGTTT CCCCCTGGAA GCTCCCTCGT GCGCTCTCCT GTTCCGACCC
       GGTCCGCAAA GGGGGACCTT CGAGGGAGCA CGCGAGAGGA CAAGGCTGGG

2951   TGCCGCTTAC CGGATACCTG TCCGCCTTTC TCCCTTCGGG AAGCGTGGCG
       ACGGCGAATG GCCTATGGAC AGGCGGAAAG AGGGAAGCCC TTCGCACCGC

3001   CTTTCTCATA GCTCACGCTG TAGGTATCTC AGTTCGGTGT AGGTCGTTCG
       GAAAGAGTAT CGAGTGCGAC ATCCATAGAG TCAAGCCACA TCCAGCAAGC

                          ApaLI
                          ~~~~~~~
3051   CTCCAAGCTG GGCTGTGTGC ACGAACCCCC CGTTCAGCCC GACCGCTGCG
       GAGGTTCGAC CCGACACACG TGCTTGGGGG GCAAGTCGGG CTGGCGACGC

3101   CCTTATCCGG TAACTATCGT CTTGAGTCCA ACCCGGTAAG ACACGACTTA
       GGAATAGGCC ATTGATAGCA GAACTCAGGT TGGGCCATTC TGTGCTGAAT
```

Fig. 12 (cont.)

```
3151  TCGCCACTGG CAGCAGCCAC TGGTAACAGG ATTAGCAGAG CGAGGTATGT
      AGCGGTGACC GTCGTCGGTG ACCATTGTCC TAATCGTCTC GCTCCATACA

3201  AGGCGGTGCT ACAGAGTTCT TGAAGTGGTG GCCTAACTAC GGCTACACTA
      TCCGCCACGA TGTCTCAAGA ACTTCACCAC CGGATTGATG CCGATGTGAT

3251  GAAGAACAGT ATTTGGTATC TGCGCTCTGC TGTAGCCAGT TACCTTCGGA
      CTTCTTGTCA TAAACCATAG ACGCGAGACG ACATCGGTCA ATGGAAGCCT

3301  AAAAGAGTTG GTAGCTCTTG ATCCGGCAAA CAAACCACCG CTGGTAGCGG
      TTTTCTCAAC CATCGAGAAC TAGGCCGTTT GTTTGGTGGC GACCATCGCC

3351  TGGTTTTTTT GTTTGCAAGC AGCAGATTAC GCGCAGAAAA AAAGGATCTC
      ACCAAAAAAA CAAACGTTCG TCGTCTAATG CGCGTCTTTT TTTCCTAGAG

3401  AAGAAGATCC TTTGATCTTT TCTACGGGGT CTGACGCTCA GTGGAACGAA
      TTCTTCTAGG AAACTAGAAA AGATGCCCCA GACTGCGAGT CACCTTGCTT

3451  AACTCACGTT AAGGGATTTT GGTCAGATCT AGCACCAGGC GTTTAAGGGC
      TTGAGTGCAA TTCCCTAAAA CCAGTCTAGA TCGTGGTCCG CAAATTCCCG

3501  ACCAATAACT GCCTTAAAAA AATTACGCCC CGCCCTGCCA CTCATCGCAG
      TGGTTATTGA CGGAATTTTT TTAATGCGGG GCGGGACGGT GAGTAGCGTC

3551  TACTGTTGTA ATTCATTAAG CATTCTGCCG ACATGGAAGC CATCACAAAC
      ATGACAACAT TAAGTAATTC GTAAGACGGC TGTACCTTCG GTAGTGTTTG

3601  GGCATGATGA ACCTGAATCG CCAGCGGCAT CAGCACCTTG TCGCCTTGCG
      CCGTACTACT TGGACTTAGC GGTCGCCGTA GTCGTGGAAC AGCGGAACGC

3651  TATAATATTT GCCCATAGTG AAAACGGGGG CGAAGAAGTT GTCCATATTG
      ATATTATAAA CGGGTATCAC TTTTGCCCCC GCTTCTTCAA CAGGTATAAC

3701  GCTACGTTTA AATCAAAACT GGTGAAACTC ACCCAGGGAT TGGCTGAGAC
      CGATGCAAAT TTAGTTTTGA CCACTTTGAG TGGGTCCCTA ACCGACTCTG

3751  GAAAAACATA TTCTCAATAA ACCCTTTAGG GAAATAGGCC AGGTTTTCAC
      CTTTTTGTAT AAGAGTTATT TGGGAAATCC CTTTATCCGG TCCAAAAGTG

3801  CGTAACACGC CACATCTTGC GAATATATGT GTAGAAACTG CCGGAAATCG
      GCATTGTGCG GTGTAGAACG CTTATATACA CATCTTTGAC GGCCTTTAGC

3851  TCGTGGTATT CACTCCAGAG CGATGAAAAC GTTTCAGTTT GCTCATGGAA
      AGCACCATAA GTGAGGTCTC GCTACTTTTG CAAAGTCAAA CGAGTACCTT

3901  AACGGTGTAA CAAGGGTGAA CACTATCCCA TATCACCAGC TCACCGTCTT
      TTGCCACATT GTTCCCACTT GTGATAGGGT ATAGTGGTCG AGTGGCAGAA

3951  TCATTGCCAT ACGGAACTCC GGGTGAGCAT TCATCAGGCG GGCAAGAATG
      AGTAACGGTA TGCCTTGAGG CCCACTCGTA AGTAGTCCGC CCGTTCTTAC
```

Fig. 12 (cont.)

```
4001   TGAATAAAGG CCGGATAAAA CTTGTGCTTA TTTTTCTTTA CGGTCTTTAA
       ACTTATTTCC GGCCTATTTT GAACACGAAT AAAAAGAAAT GCCAGAAATT

4051   AAAGGCCGTA ATATCCAGCT GAACGGTCTG GTTATAGGTA CATTGAGCAA
       TTTCCGGCAT TATAGGTCGA CTTGCCAGAC CAATATCCAT GTAACTCGTT

4101   CTGACTGAAA TGCCTCAAAA TGTTCTTTAC GATGCCATTG GGATATATCA
       GACTGACTTT ACGGAGTTTT ACAAGAAATG CTACGGTAAC CCTATATAGT

4151   ACGGTGGTAT ATCCAGTGAT TTTTTTCTCC ATTTTAGCTT CCTTAGCTCC
       TGCCACCATA TAGGTCACTA AAAAAAGAGG TAAAATCGAA GGAATCGAGG

4201   TGAAAATCTC GATAACTCAA AAAATACGCC CGGTAGTGAT CTTATTTCAT
       ACTTTTAGAG CTATTGAGTT TTTTATGCGG GCCATCACTA GAATAAAGTA

4251   TATGGTGAAA GTTGGAACCT CACCCGACGT CTAATGTGAG TTAGCTCACT
       ATACCACTTT CAACCTTGGA GTGGGCTGCA GATTACACTC AATCGAGTGA

4301   CATTAGGCAC CCCAGGCTTT ACACTTTATG CTTCCGGCTC GTATGTTGTG
       GTAATCCGTG GGGTCCGAAA TGTGAAATAC GAAGGCCGAG CATACAACAC

                                          M13 Reverse primer 100.0%
                                          ==================
4351   TGGAATTGTG AGCGGATAAC AATTTCACAC AGGAAACAGC TATGACCATG
       ACCTTAACAC TCGCCTATTG TTAAAGTGTG TCCTTTGTCG ATACTGGTAC

4401   ATTACGAATT
       TAATGCTTAA
```

Fig. 12 (cont.)

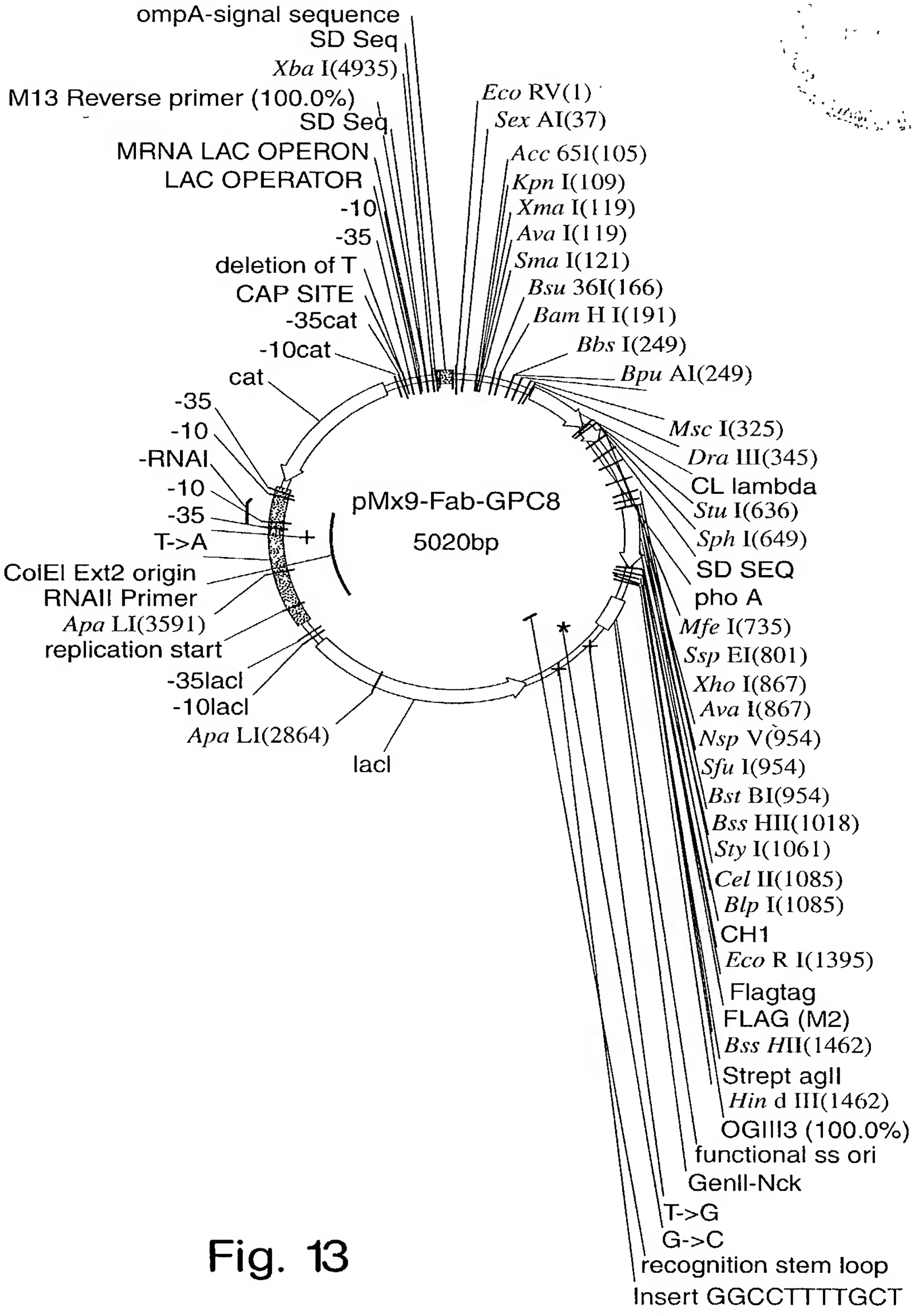
pMx9-Fab-GPC8
5020bp
ompA-signal sequence
SD Seq
Xba I(4935)
M13 Reverse primer (100.0%)
SD Seq
MRNA LAC OPERON
LAC OPERATOR
-10
-35
deletion of T
CAP SITE
-35cat
-10cat
cat
-35
-10
-RNAI
-10
-35
T->A
ColEI Ext2 origin
RNAII Primer
Apa LI(3591)
replication start
-35lacI
-10lacI
Apa LI(2864)
lacI
Eco RV(1)
Sex AI(37)
Acc 65I(105)
Kpn I(109)
Xma I(119)
Ava I(119)
Sma I(121)
Bsu 36I(166)
Bam H I(191)
Bbs I(249)
Bpu AI(249)
Msc I(325)
Dra III(345)
CL lambda
Stu I(636)
Sph I(649)
SD SEQ
pho A
Mfe I(735)
Ssp EI(801)
Xho I(867)
Ava I(867)
Nsp V(954)
Sfu I(954)
Bst BI(954)
Bss HII(1018)
Sty I(1061)
Cel II(1085)
Blp I(1085)
CH1
Eco R I(1395)
Flagtag
FLAG (M2)
Bss HII(1462)
Strept agII
Hin d III(1462)
OGIII3 (100.0%)
functional ss ori
GenII-Nck
T->G
G->C
recognition stem loop
Insert GGCCTTTTGCT

Fig. 13

```
      EcoRV                                                    SexAI
      ~~~                                                      ~~~~~~~~
  1   ATCGTGCTGA CCCAGCCGCC TTCAGTGAGT GGCGCACCAG GTCAGCGTGT
      TAGCACGACT GGGTCGGCGG AAGTCACTCA CCGCGTGGTC CAGTCGCACA

 51   GACCATCTCG TGTAGCGGCA GCAGCAGCAA CATTGGCAGC AACTATGTGA
      CTGGTAGAGC ACATCGCCGT CGTCGTCGTT GTAACCGTCG TTGATACACT

                          XmaI
                          ~~~~~~~
            KpnI          SmaI
            ~~~~~~        ~~~~~~~
          Acc65I          AvaI
            ~~~~~~        ~~~~~~~
101   GCTGGTACCA GCAGTTGCCC GGGACGGCGC CGAAACTGCT GATTTATGAT
      CGACCATGGT CGTCAACGGG CCCTGCCGCG GCTTTGACGA CTAAATACTA

                    Bsu36I                                  BamHI
                    ~~~~~~~                                 ~~~~~~~
151   AACAACCAGC GTCCCTCAGG CGTGCCGGAT CGTTTTAGCG GATCCAAAAG
      TTGTTGGTCG CAGGGAGTCC GCACGGCCTA GCAAAATCGC CTAGGTTTTC

                                                             BpuAI
                                                             ~~~~~~
                                                             BbsI
                                                             ~~~~~~
201   CGGCACCAGC GCGAGCCTTG CGATTACGGG CCTGCAAAGC GAAGACGAAG
      GCCGTGGTCG CGCTCGGAAC GCTAATGCCC GGACGTTTCG CTTCTGCTTC

                                      Bsu36I
                                      ~~~~~~~~
251   CGGATTATTA TTGCCAGAGC TATGACATGC CTCAGGCTGT GTTTGGCGGC
      GCCTAATAAT AACGGTCTCG ATACTGTACG GAGTCCGACA CAAACCGCCG

                                MscI                  DraIII
                                ~~~~~~                ~~~~~~~~~~
301   GGCACGAAGT TTAACCGTTC TTGGCCAGCC GAAAGCCGCA CCGAGTGTGA
      CCGTGCTTCA AATTGGCAAG AACCGGTCGG CTTTCGGCGT GGCTCACACT

351   CGCTGTTTCC GCCGAGCAGC GAAGAATTGC AGGCGAACAA AGCGACCCTG
      GCGACAAAGG CGGCTCGTCG CTTCTTAACG TCCGCTTGTT TCGCTGGGAC

401   GTGTGCCTGA TTAGCGACTT TTATCCGGGA GCCGTGACAG TGGCCTGGAA
      CACACGGACT AATCGCTGAA AATAGGCCCT CGGCACTGTC ACCGGACCTT

451   GGCAGATAGC AGCCCCGTCA AGGCGGGAGT GGAGACCACC ACACCCTCCA
      CCGTCTATCG TCGGGGCAGT TCCGCCCTCA CCTCTGGTGG TGTGGGAGGT

501   AACAAAGCAA CAACAAGTAC GCGGCCAGCA GCTATCTGAG CCTGACGCCT
      TTGTTTCGTT GTTGTTCATG CGCCGGTCGT CGATAGACTC GGACTGCGGA
```

Fig. 13 (cont.)

```
551   GAGCAGTGGA AGTCCCACAG AAGCTACAGC TGCCAGGTCA CGCATGAGGG
      CTCGTCACCT TCAGGGTGTC TTCGATGTCG ACGGTCCAGT GCGTACTCCC

                                          StuI       SphI
                                          ~~~~~~     ~~~~~~
601   GAGCACCGTG GAAAAAACCG TTGCGCCGAC TGAGGCCTGA TAAGCATGCG
      CTCGTGGCAC CTTTTTTGGC AACGCGGCTG ACTCCGGACT ATTCGTACGC

651   TAGGAGAAAA TAAAATGAAA CAAAGCACTA TTGCACTGGC ACTCTTACCG
      ATCCTCTTTT ATTTTACTTT GTTTCGTGAT AACGTGACCG TGAGAATGGC

                                          MfeI
                                          ~~~~~~
701   TTGCTCTTCA CCCCTGTTAC CAAAGCCCAG GTGCAATTGA AAGAAAGCGG
      AACGAGAAGT GGGGACAATG GTTTCGGGTC CACGTTAACT TTCTTTCGCC

                                                      BspEI
                                                      ~
751   CCCGGCCCTG GTGAAACCGA CCCAAACCCT GACCCTGACC TGTACCTTTT
      GGGCCGGGAC CACTTTGGCT GGGTTTGGGA CTGGGACTGG ACATGGAAAA

      BspEI
      ~~~~~
801   CCGGATTTAG CCTGTCCACG TCTGGCGTTG GCGTGGGCTG GATTCGCCAG
      GGCCTAAATC GGACAGGTGC AGACCGCAAC CGCACCCGAC CTAAGCGGTC

                        XhoI
                        ~~~~~~~
                        AvaI
                        ~~~~~~~
851   CCGCCTGGGA AAGCCCTCGA GTGGCTGGCT CTGATTGATT GGGATGATGA
      GGCGGACCCT TTCGGGAGCT CACCGACCGA GACTAACTAA CCCTACTACT

901   TAAGTATTAT AGCACCAGCC TGAAAACGCG TCTGACCATT AGCAAAGATA
      ATTCATAATA TCGTGGTCGG ACTTTTGCGC AGACTGGTAA TCGTTTCTAT

        BstBI
        ~~~~~~
        SfuI
        ~~~~~~
        NspV
        ~~~~~~
951   CTTCGAAAAA TCAGGTGGTG CTGACTATGA CCAACATGGA CCCGGTGGAT
      GAAGCTTTTT AGTCCACCAC GACTGATACT GGTTGTACCT GGGCCACCTA

                          BssHII
                          ~~~~~~~
1001  ACGGCCACCT ATTATTGCGC GCGTTCTCCT CGTTATCGTG GTGCTTTTGA
      TGCCGGTGGA TAATAACGCG CGCAAGAGGA GCAATAGCAC CACGAAAACT

                                                BlpI
```

Fig. 13 (cont.)

```
                                              ~~~~~~~~
                StyI                           CelII
              ~~~~~~~~                        ~~~~~~~~
1051  TTATTGGGGC CAAGGCACCC TGGTGACGGT TAGCTCAGCG TCGACCAAAG
      AATAACCCCG GTTCCGTGGG ACCACTGCCA ATCGAGTCGC AGCTGGTTTC

1101  GTCCAAGCGT GTTTCCGCTG GCTCCGAGCA GCAAAAGCAC CAGCGGCGGC
      CAGGTTCGCA CAAAGGCGAC CGAGGCTCGT CGTTTTCGTG GTCGCCGCCG

1151  ACGGCTGCCC TGGGCTGCCT GGTTAAAGAT TATTTCCCGG AACCAGTCAC
      TGCCGACGGG ACCCGACGGA CCAATTTCTA ATAAAGGGCC TTGGTCAGTG

1201  CGTGAGCTGG AACAGCGGGG CGCTGACCAG CGGCGTGCAT ACCTTTCCGG
      GCACTCGACC TTGTCGCCCC GCGACTGGTC GCCGCACGTA TGGAAAGGCC

1251  CGGTGCTGCA AAGCAGCGGC CTGTATAGCC TGAGCAGCGT TGTGACCGTG
      GCCACGACGT TTCGTCGCCG GACATATCGG ACTCGTCGCA ACACTGGCAC

1301  CCGAGCAGCA GCTTAGGCAC TCAGACCTAT ATTTGCAACG TGAACCATAA
      GGCTCGTCGT CGAATCCGTG AGTCTGGATA TAAACGTTGC ACTTGGTATT

                                                   EcoRI
                                                  ~~~~~~
1351  ACCGAGCAAC ACCAAAGTGG ATAAAAAAGT GGAACCGAAA AGCGAATTCG
      TGGCTCGTTG TGGTTTCACC TATTTTTTCA CCTTGGCTTT TCGCTTAAGC

                                BssHII
                                ~~~~~~
1401  ACTATAAAGA TGACGATGAC AAAGGCGCGC CGTGGAGCCA CCCGCAGTTT
      TGATATTTCT ACTGCTACTG TTTCCGCGCG GCACCTCGGT GGGCGTCAAA

                 HindIII
                 ~~~~~~
1451  GAAAAATGAT AAGCTTGACC TGTGAAGTGA AAAATGGCGC AGATTGTGCG
      CTTTTTACTA TTCGAACTGG ACACTTCACT TTTTACCGCG TCTAACACGC
                            OGIII3   100.0%
                         ====================

1501  ACATTTTTTT TGTCTGCCGT TTAATTAAAG GGGGGGGGGG GCCGGCCTGG
      TGTAAAAAAA ACAGACGGCA AATTAATTTC CCCCCCCCCC CGGCCGGACC

1551  GGGGGGGTGT ACATGAAATT GTAAACGTTA ATATTTTGTT AAAATTCGCG
      CCCCCCCACA TGTACTTTAA CATTTGCAAT TATAAAACAA TTTTAAGCGC

1601  TTAAATTTTT GTTAAATCAG CTCATTTTTT AACCAATAGG CCGAAATCGG
      AATTTAAAAA CAATTTAGTC GAGTAAAAAA TTGGTTATCC GGCTTTAGCC

1651  CAAAATCCCT TATAAATCAA AAGAATAGAC CGAGATAGGG TTGAGTGTTG
      GTTTTAGGGA ATATTTAGTT TTCTTATCTG GCTCTATCCC AACTCACAAC

1701  TTCCAGTTTG GAACAAGAGT CCACTATTAA AGAACGTGGA CTCCAACGTC
      AAGGTCAAAC CTTGTTCTCA GGTGATAATT TCTTGCACCT GAGGTTGCAG
```

Fig. 13 (cont.)

```
1751  AAAGGGCGAA AAACCGTCTA TCAGGGCGAT GGCCCACTAC GAGAACCATC
      TTTCCCGCTT TTTGGCAGAT AGTCCCGCTA CCGGGTGATG CTCTTGGTAG

1801  ACCCTAATCA AGTTTTTTGG GGTCGAGGTG CCGTAAAGCA CTAAATCGGA
      TGGGATTAGT TCAAAAAACC CCAGCTCCAC GGCATTTCGT GATTTAGCCT

1851  ACCCTAAAGG GAGCCCCCGA TTTAGAGCTT GACGGGGAAA GCCGGCGAAC
      TGGGATTTCC CTCGGGGGCT AAATCTCGAA CTGCCCCTTT CGGCCGCTTG

1901  GTGGCGAGAA AGGAAGGGAA GAAAGCGAAA GGAGCGGGCG CTAGGGCGCT
      CACCGCTCTT TCCTTCCCTT CTTTCGCTTT CCTCGCCCGC GATCCCGCGA

1951  GGCAAGTGTA GCGGTCACGC TGCGCGTAAC CACCACACCC GCCGCGCTTA
      CCGTTCACAT CGCCAGTGCG ACGCGCATTG GTGGTGTGGG CGGCGCGAAT

2001  ATGCGCCGCT ACAGGGCGCG TGCTAGACTA GTGTTTAAAC CGGACCGGGG
      TACGCGGCGA TGTCCCGCGC ACGATCTGAT CACAAATTTG GCCTGGCCCC

2051  GGGGGCTTAA GTGGGCTGCA AAACAAAACG GCCTCCTGTC AGGAAGCCGC
      CCCCCGAATT CACCCGACGT TTTGTTTTGC CGGAGGACAG TCCTTCGGCG

2101  TTTTATCGGG TAGCCTCACT GCCCGCTTTC CAGTCGGGAA ACCTGTCGTG
      AAAATAGCCC ATCGGAGTGA CGGGCGAAAG GTCAGCCCTT TGGACAGCAC

2151  CCAGCTGCAT CAGTGAATCG GCCAACGCGC GGGGAGAGGC GGTTTGCGTA
      GGTCGACGTA GTCACTTAGC CGGTTGCGCG CCCCTCTCCG CCAAACGCAT

2201  TTGGGAGCCA GGGTGGTTTT TCTTTTCACC AGTGAGACGG GCAACAGCTG
      AACCCTCGGT CCCACCAAAA AGAAAAGTGG TCACTCTGCC CGTTGTCGAC

2251  ATTGCCCTTC ACCGCCTGGC CCTGAGAGAG TTGCAGCAAG CGGTCCACGC
      TAACGGGAAG TGGCGGACCG GGACTCTCTC AACGTCGTTC GCCAGGTGCG

2301  TGGTTTGCCC CAGCAGGCGA AAATCCTGTT TGATGGTGGT CAGCGGCGGG
      ACCAAACGGG GTCGTCCGCT TTTAGGACAA ACTACCACCA GTCGCCGCCC

2351  ATATAACATG AGCTGTCCTC GGTATCGTCG TATCCCACTA CCGAGATGTC
      TATATTGTAC TCGACAGGAG CCATAGCAGC ATAGGGTGAT GGCTCTACAG

2401  CGCACCAACG CGCAGCCCGG ACTCGGTAAT GGCACGCATT GCGCCCAGCG
      GCGTGGTTGC GCGTCGGGCC TGAGCCATTA CCGTGCGTAA CGCGGGTCGC

2451  CCATCTGATC GTTGGCAACC AGCATCGCAG TGGGAACGAT GCCCTCATTC
      GGTAGACTAG CAACCGTTGG TCGTAGCGTC ACCCTTGCTA CGGGAGTAAG

2501  AGCATTTGCA TGGTTTGTTG AAAACCGGAC ATGGCACTCC AGTCGCCTTC
      TCGTAAACGT ACCAAACAAC TTTTGGCCTG TACCGTGAGG TCAGCGGAAG

2551  CCGTTCCGCT ATCGGCTGAA TTTGATTGCG AGTGAGATAT TTATGCCAGC
      GGCAAGGCGA TAGCCGACTT AAACTAACGC TCACTCTATA AATACGGTCG
```

Fig. 13 (cont.)

```
2601   CAGCCAGACG CAGACGCGCC GAGACAGAAC TTAATGGGCC AGCTAACAGC
       GTCGGTCTGC GTCTGCGCGG CTCTGTCTTG AATTACCCGG TCGATTGTCG

2651   GCGATTTGCT GGTGGCCCAA TGCGACCAGA TGCTCCACGC CCAGTCGCGT
       CGCTAAACGA CCACCGGGTT ACGCTGGTCT ACGAGGTGCG GGTCAGCGCA

2701   ACCGTCCTCA TGGGAGAAAA TAATACTGTT GATGGGTGTC TGGTCAGAGA
       TGGCAGGAGT ACCCTCTTTT ATTATGACAA CTACCCACAG ACCAGTCTCT

2751   CATCAAGAAA TAACGCCGGA ACATTAGTGC AGGCAGCTTC CACAGCAATA
       GTAGTTCTTT ATTGCGGCCT TGTAATCACG TCCGTCGAAG GTGTCGTTAT

2801   GCATCCTGGT CATCCAGCGG ATAGTTAATA ATCAGCCCAC TGACACGTTG
       CGTAGGACCA GTAGGTCGCC TATCAATTAT TAGTCGGGTG ACTGTGCAAC

                    ApaLI
                    ~~~~~~
2851   CGCGAGAAGA TTGTGCACCG CCGCTTTACA GGCTTCGACG CCGCTTCGTT
       GCGCTCTTCT AACACGTGGC GGCGAAATGT CCGAAGCTGC GGCGAAGCAA

2901   CTACCATCGA CACGACCACG CTGGCACCCA GTTGATCGGC GCGAGATTTA
       GATGGTAGCT GTGCTGGTGC GACCGTGGGT CAACTAGCCG CGCTCTAAAT

2951   ATCGCCGCGA CAATTTGCGA CGGCGCGTGC AGGGCCAGAC TGGAGGTGGC
       TAGCGGCGCT GTTAAACGCT GCCGCGCACG TCCCGGTCTG ACCTCCACCG

3001   AACGCCAATC AGCAACGACT GTTTGCCCGC CAGTTGTTGT GCCACGCGGT
       TTGCGGTTAG TCGTTGCTGA CAAACGGGCG GTCAACAACA CGGTGCGCCA

3051   TAGGAATGTA ATTCAGCTCC GCCATCGCCG CTTCCACTTT TTCCCGCGTT
       ATCCTTACAT TAAGTCGAGG CGGTAGCGGC GAAGGTGAAA AAGGGCGCAA

3101   TTCGCAGAAA CGTGGCTGGC CTGGTTCACC ACGCGGGAAA CGGTCTGATA
       AAGCGTCTTT GCACCGACCG GACCAAGTGG TGCGCCCTTT GCCAGACTAT

3151   AGAGACACCG GCATACTCTG CGACATCGTA TAACGTTACT GGTTTCACAT
       TCTCTGTGGC CGTATGAGAC GCTGTAGCAT ATTGCAATGA CCAAAGTGTA

3201   TCACCACCCT GAATTGACTC TCTTCCGGGC GCTATCATGC CATACCGCGA
       AGTGGTGGGA CTTAACTGAG AGAAGGCCCG CGATAGTACG GTATGGCGCT

3251   AAGGTTTTGC GCCATTCGAT GCTAGCCATG TGAGCAAAAG GCCAGCAAAA
       TTCCAAAACG CGGTAAGCTA CGATCGGTAC ACTCGTTTTC CGGTCGTTTT

3301   GGCCAGGAAC CGTAAAAAGG CCGCGTTGCT GGCGTTTTTC CATAGGCTCC
       CCGGTCCTTG GCATTTTTCC GGCGCAACGA CCGCAAAAAG GTATCCGAGG

3351   GCCCCCCTGA CGAGCATCAC AAAAATCGAC GCTCAAGTCA GAGGTGGCGA
       CGGGGGGACT GCTCGTAGTG TTTTTAGCTG CGAGTTCAGT CTCCACCGCT

3401   AACCCGACAG GACTATAAAG ATACCAGGCG TTTCCCCCTG GAAGCTCCCT
```

Fig. 13 (cont.)

```
        TTGGGCTGTC CTGATATTTC TATGGTCCGC AAAGGGGGAC CTTCGAGGGA

3451    CGTGCGCTCT CCTGTTCCGA CCCTGCCGCT TACCGGATAC CTGTCCGCCT
        GCACGCGAGA GGACAAGGCT GGGACGGCGA ATGGCCTATG GACAGGCGGA

3501    TTCTCCCTTC GGGAAGCGTG GCGCTTTCTC ATAGCTCACG CTGTAGGTAT
        AAGAGGGAAG CCCTTCGCAC CGCGAAAGAG TATCGAGTGC GACATCCATA

                                                      ApaLI
                                                    ~~~~~~~~
3551    CTCAGTTCGG TGTAGGTCGT TCGCTCCAAG CTGGGCTGTG TGCACGAACC
        GAGTCAAGCC ACATCCAGCA AGCGAGGTTC GACCCGACAC ACGTGCTTGG

3601    CCCCGTTCAG CCCGACCGCT GCGCCTTATC CGGTAACTAT CGTCTTGAGT
        GGGGCAAGTC GGGCTGGCGA CGCGGAATAG GCCATTGATA GCAGAACTCA

3651    CCAACCCGGT AAGACACGAC TTATCGCCAC TGGCAGCAGC CACTGGTAAC
        GGTTGGGCCA TTCTGTGCTG AATAGCGGTG ACCGTCGTCG GTGACCATTG

3701    AGGATTAGCA GAGCGAGGTA TGTAGGCGGT GCTACAGAGT TCTTGAAGTG
        TCCTAATCGT CTCGCTCCAT ACATCCGCCA CGATGTCTCA AGAACTTCAC

3751    GTGGCCTAAC TACGGCTACA CTAGAAGAAC AGTATTTGGT ATCTGCGCTC
        CACCGGATTG ATGCCGATGT GATCTTCTTG TCATAAACCA TAGACGCGAG

3801    TGCTGTAGCC AGTTACCTTC GGAAAAAGAG TTGGTAGCTC TTGATCCGGC
        ACGACATCGG TCAATGGAAG CCTTTTTCTC AACCATCGAG AACTAGGCCG

3851    AAACAAACCA CCGCTGGTAG CGGTGGTTTT TTTGTTTGCA AGCAGCAGAT
        TTTGTTTGGT GGCGACCATC GCCACCAAAA AAACAAACGT TCGTCGTCTA

3901    TACGCGCAGA AAAAAAGGAT CTCAAGAAGA TCCTTTGATC TTTTCTACGG
        ATGCGCGTCT TTTTTTCCTA GAGTTCTTCT AGGAAACTAG AAAAGATGCC

3951    GGTCTGACGC TCAGTGGAAC GAAAACTCAC GTTAAGGGAT TTTGGTCAGA
        CCAGACTGCG AGTCACCTTG CTTTTGAGTG CAATTCCCTA AAACCAGTCT

4001    TCTAGCACCA GGCGTTTAAG GGCACCAATA ACTGCCTTAA AAAAATTACG
        AGATCGTGGT CCGCAAATTC CCGTGGTTAT TGACGGAATT TTTTTAATGC

4051    CCCCGCCCTG CCACTCATCG CAGTACTGTT GTAATTCATT AAGCATTCTG
        GGGGCGGGAC GGTGAGTAGC GTCATGACAA CATTAAGTAA TTCGTAAGAC

4101    CCGACATGGA AGCCATCACA AACGGCATGA TGAACCTGAA TCGCCAGCGG
        GGCTGTACCT TCGGTAGTGT TTGCCGTACT ACTTGGACTT AGCGGTCGCC

4151    CATCAGCACC TTGTCGCCTT GCGTATAATA TTTGCCCATA GTGAAAACGG
        GTAGTCGTGG AACAGCGGAA CGCATATTAT AAACGGGTAT CACTTTTGCC

4201    GGGCGAAGAA GTTGTCCATA TTGGCTACGT TTAAATCAAA ACTGGTGAAA
        CCCGCTTCTT CAACAGGTAT AACCGATGCA AATTTAGTTT TGACCACTTT
```

Fig. 13 (cont.)

```
4251  CTCACCCAGG GATTGGCTGA GACGAAAAAC ATATTCTCAA TAAACCCTTT
      GAGTGGGTCC CTAACCGACT CTGCTTTTTG TATAAGAGTT ATTTGGGAAA

4301  AGGGAAATAG GCCAGGTTTT CACCGTAACA CGCCACATCT TGCGAATATA
      TCCCTTTATC CGGTCCAAAA GTGGCATTGT GCGGTGTAGA ACGCTTATAT

4351  TGTGTAGAAA CTGCCGGAAA TCGTCGTGGT ATTCACTCCA GAGCGATGAA
      ACACATCTTT GACGGCCTTT AGCAGCACCA TAAGTGAGGT CTCGCTACTT

4401  AACGTTTCAG TTTGCTCATG GAAAACGGTG TAACAAGGGT GAACACTATC
      TTGCAAAGTC AAACGAGTAC CTTTTGCCAC ATTGTTCCCA CTTGTGATAG

4451  CCATATCACC AGCTCACCGT CTTTCATTGC CATACGGAAC TCCGGGTGAG
      GGTATAGTGG TCGAGTGGCA GAAAGTAACG GTATGCCTTG AGGCCCACTC

4501  CATTCATCAG GCGGGCAAGA ATGTGAATAA AGGCCGGATA AAACTTGTGC
      GTAAGTAGTC CGCCCGTTCT TACACTTATT TCCGGCCTAT TTTGAACACG

4551  TTATTTTTCT TTACGGTCTT TAAAAAGGCC GTAATATCCA GCTGAACGGT
      AATAAAAAGA AATGCCAGAA ATTTTTCCGG CATTATAGGT CGACTTGCCA

4601  CTGGTTATAG GTACATTGAG CAACTGACTG AAATGCCTCA AAATGTTCTT
      GACCAATATC CATGTAACTC GTTGACTGAC TTTACGGAGT TTTACAAGAA

4651  TACGATGCCA TTGGGATATA TCAACGGTGG TATATCCAGT GATTTTTTTC
      ATGCTACGGT AACCCTATAT AGTTGCCACC ATATAGGTCA CTAAAAAAAG

4701  TCCATTTTAG CTTCCTTAGC TCCTGAAAAT CTCGATAACT CAAAAAATAC
      AGGTAAAATC GAAGGAATCG AGGACTTTTA GAGCTATTGA GTTTTTTATG

4751  GCCCGGTAGT GATCTTATTT CATTATGGTG AAAGTTGGAA CCTCACCCGA
      CGGGCCATCA CTAGAATAAA GTAATACCAC TTTCAACCTT GGAGTGGGCT

4801  CGTCTAATGT GAGTTAGCTC ACTCATTAGG CACCCCAGGC TTTACACTTT
      GCAGATTACA CTCAATCGAG TGAGTAATCC GTGGGGTCCG AAATGTGAAA

4851  ATGCTTCCGG CTCGTATGTT GTGTGGAATT GTGAGCGGAT AACAATTTCA
      TACGAAGGCC GAGCATACAA CACACCTTAA CACTCGCCTA TTGTTAAAGT

      M13 Reverse  primer 100.0%              XbaI
      ====================                    ~~~~~~~

4901  CACAGGAAAC AGCTATGACC ATGATTACGA ATTTCTAGAT AACGAGGGCA
      GTGTCCTTTG TCGATACTGG TACTAATGCT TAAAGATCTA TTGCTCCCGT

4951  AAAAATGAAA AAGACAGCTA TCGCGATTGC AGTGGCACTG GCTGGTTTCG
      TTTTTACTTT TTCTGTCGAT AGCGCTAACG TCACCGTGAC CGACCAAAGC

                          EcoRV
                           ~~~
5001  CTACCGTAGC GCAGGCCGAT
      GATGGCATCG CGTCCGGCTA
```

Fig. 13 (cont.)

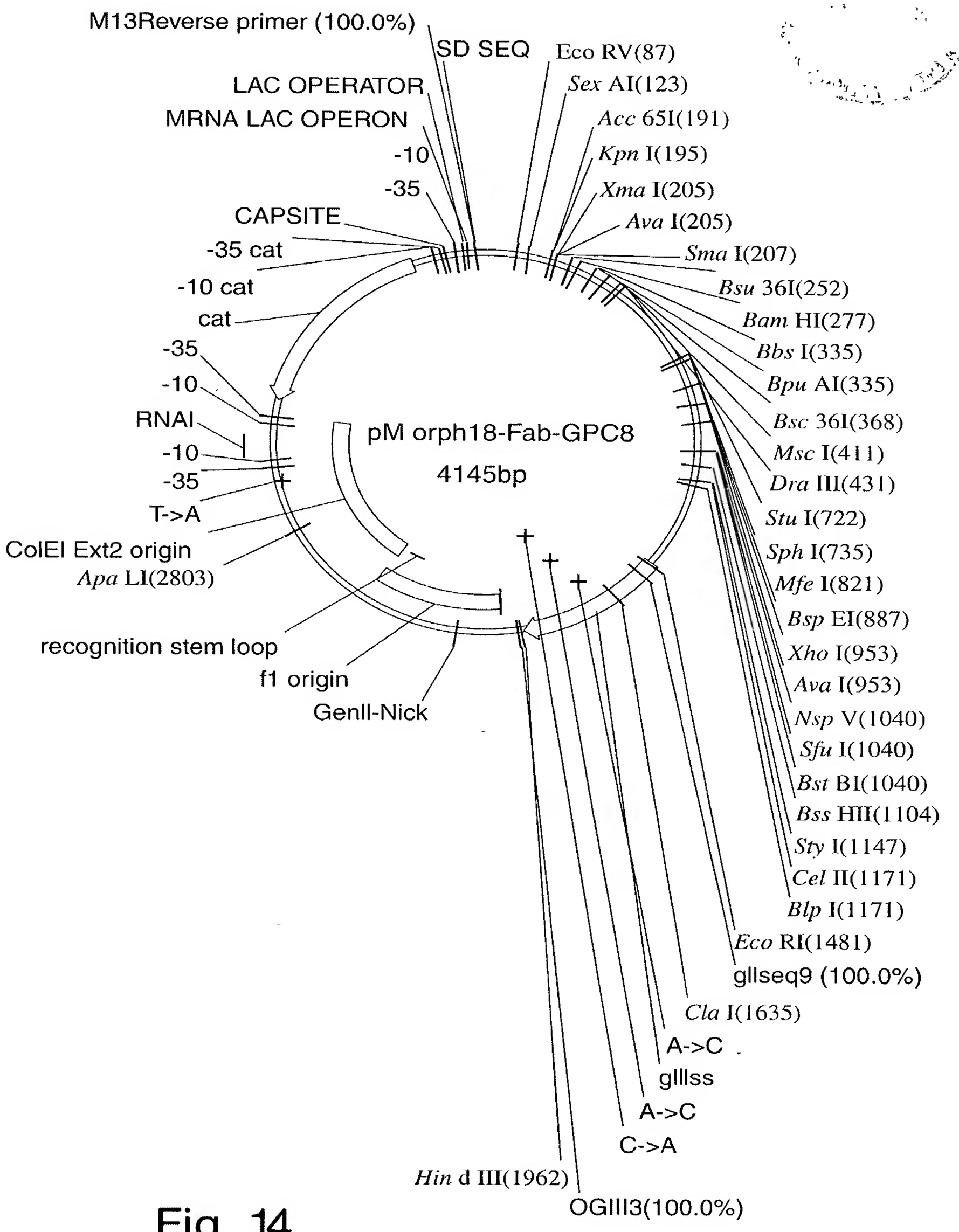
M13Reverse primer (100.0%)
SD SEQ
LAC OPERATOR
MRNA LAC OPERON
-10
-35
CAPSITE
-35 cat
-10 cat
cat
-35
-10
RNAI
-10
-35
T->A
ColEI Ext2 origin
Apa LI(2803)
recognition stem loop
f1 origin
GenII-Nick
pM orph18-Fab-GPC8
4145bp
Eco RV(87)
Sex AI(123)
Acc 65I(191)
Kpn I(195)
Xma I(205)
Ava I(205)
Sma I(207)
Bsu 36I(252)
Bam HI(277)
Bbs I(335)
Bpu AI(335)
Bsc 36I(368)
Msc I(411)
Dra III(431)
Stu I(722)
Sph I(735)
Mfe I(821)
Bsp EI(887)
Xho I(953)
Ava I(953)
Nsp V(1040)
Sfu I(1040)
Bst BI(1040)
Bss HII(1104)
Sty I(1147)
Cel II(1171)
Blp I(1171)
Eco RI(1481)
gIIseq9 (100.0%)
Cla I(1635)
A->C
gIIIss
A->C
C->A
Hin d III(1962)
OGIII3(100.0%)

Fig. 14

```
  1  TCAGATAACG AGGGCAAAAA ATGAAAAAGA CAGCTATCGC GATTGCAGTG
     AGTCTATTGC TCCCGTTTTT TACTTTTTCT GTCGATAGCG CTAACGTCAC

                                       EcoRV
                                      ~~~~~~
 51  GCACTGGCTG GTTTCGCTAC CGTAGCGCAG GCCGATATCG TGCTGACCCA
     CGTGACCGAC CAAAGCGATG GCATCGCGTC CGGCTATAGC ACGACTGGGT

                            SexAI
                           ~~~~~~~
101  GCCGCCTTCA GTGAGTGGCG CACCAGGTCA GCGTGTGACC ATCTCGTGTA
     CGGCGGAAGT CACTCACCGC GTGGTCCAGT CGCACACTGG TAGAGCACAT

                                                  KpnI
                                                ~~~~~~~
                                                Acc65I
                                                ~~~~~~~
151  GCGGCAGCAG CAGCAACATT GGCAGCAACT ATGTGAGCTG GTACCAGCAG
     CGCCGTCGTC GTCGTTGTAA CCGTCGTTGA TACACTCGAC CATGGTCGTC

        XmaI
       ~~~~~~
        SmaI
       ~~~~~~
        AvaI                                       Bsu36I
       ~~~~~~                                           ~
201  TTGCCCGGGA CGGCGCCGAA ACTGCTGATT TATGATAACA ACCAGCGTCC
     AACGGGCCCT GCCGCGGCTT TGACGACTAA ATACTATTGT TGGTCGCAGG

     Bsu36I                    BamHI
     ~~~~~~                   ~~~~~~~
251  CTCAGGCGTG CCGGATCGTT TTAGCGGATC CAAAAGCGGC ACCAGCGCGA
     GAGTCCGCAC GGCCTAGCAA AATCGCCTAG GTTTTCGCCG TGGTCGCGCT

                                BpuAI
                               ~~~~~~~
                                BbsI
                               ~~~~~~~
301  GCCTTGCGAT TACGGGCCTG CAAAGCGAAG ACGAAGCGGA TTATTATTGC
     CGGAACGCTA ATGCCCGGAC GTTTCGCTTC TGCTTCGCCT AATAATAACG

                     Bsu36I
                    ~~~~~~~~
351  CAGAGCTATG ACATGCCTCA GGCTGTGTTT GGCGGCGGCA CGAAGTTTAA
     GTCTCGATAC TGTACGGAGT CCGACACAAA CCGCCGCCGT GCTTCAAATT

              MscI              DraIII
             ~~~~~~~          ~~~~~~~~~~
401  CCGTTCTTGG CCAGCCGAAA GCCGCACCGA GTGTGACGCT GTTTCCGCCG
     GGCAAGAACC GGTCGGCTTT CGGCGTGGCT CACACTGCGA CAAAGGCGGC

451  AGCAGCGAAG AATTGCAGGC GAACAAAGCG ACCCTGGTGT GCCTGATTAG
     TCGTCGCTTC TTAACGTCCG CTTGTTTCGC TGGGACCACA CGGACTAATC

501  CGACTTTTAT CCGGGAGCCG TGACAGTGGC CTGGAAGGCA GATAGCAGCC
```

Fig. 14 (cont.)

```
        GCTGAAAATA GGCCCTCGGC ACTGTCACCG GACCTTCCGT CTATCGTCGG

551     CCGTCAAGGC GGGAGTGGAG ACCACCACAC CCTCCAAACA AAGCAACAAC
        GGCAGTTCCG CCCTCACCTC TGGTGGTGTG GGAGGTTTGT TTCGTTGTTG

601     AAGTACGCGG CCAGCAGCTA TCTGAGCCTG ACGCCTGAGC AGTGGAAGTC
        TTCATGCGCC GGTCGTCGAT AGACTCGGAC TGCGGACTCG TCACCTTCAG

651     CCACAGAAGC TACAGCTGCC AGGTCACGCA TGAGGGGAGC ACCGTGGAAA
        GGTGTCTTCG ATGTCGACGG TCCAGTGCGT ACTCCCCTCG TGGCACCTTT

                              StuI          SphI
                            ~~~~~~~       ~~~~~~~
701     AAACCGTTGC GCCGACTGAG GCCTGATAAG CATGCGTAGG AGAAAATAAA
        TTTGGCAACG CGGCTGACTC CGGACTATTC GTACGCATCC TCTTTTATTT

751     ATGAAACAAA GCACTATTGC ACTGGCACTC TTACCGTTGC TCTTCACCCC
        TACTTTGTTT CGTGATAACG TGACCGTGAG AATGGCAACG AGAAGTGGGG

                                  MfeI
                                ~~~~~~~
801     TGTTACCAAA GCCCAGGTGC AATTGAAAGA AAGCGGCCCG GCCCTGGTGA
        ACAATGGTTT CGGGTCCACG TTAACTTTCT TTCGCCGGGC CGGGACCACT

                                                    BspEI
                                                  ~~~~~~~
851     AACCGACCCA AACCCTGACC CTGACCTGTA CCTTTTCCGG ATTTAGCCTG
        TTGGCTGGGT TTGGGACTGG GACTGGACAT GGAAAAGGCC TAAATCGGAC

901     TCCACGTCTG GCGTTGGCGT GGGCTGGATT CGCCAGCCGC CTGGGAAAGC
        AGGTGCAGAC CGCAACCGCA CCCGACCTAA GCGGTCGGCG GACCCTTTCG

          XhoI
        ~~~~~~
          AvaI
        ~~~~~~
951     CCTCGAGTGG CTGGCTCTGA TTGATTGGGA TGATGATAAG TATTATAGCA
        GGAGCTCACC GACCGAGACT AACTAACCCT ACTACTATTC ATAATATCGT

                                                      BstBI
                                                    ~~~~~~~
                                                     SfuI
                                                    ~~~~~~~
                                                     NspV
                                                    ~~~~~~~
1001    CCAGCCTGAA AACGCGTCTG ACCATTAGCA AAGATACTTC GAAAAATCAG
        GGTCGGACTT TTGCGCAGAC TGGTAATCGT TTCTATGAAG CTTTTTAGTC

1051    GTGGTGCTGA CTATGACCAA CATGGACCCG GTGGATACGG CCACCTATTA
        CACCACGACT GATACTGGTT GTACCTGGGC CACCTATGCC GGTGGATAAT

          BssHII                                              StyI
        ~~~~~~                                              ~~~~~
1101    TTGCGCGCGT TCTCCTCGTT ATCGTGGTGC TTTTGATTAT TGGGGCCAAG
        AACGCGCGCA AGAGGAGCAA TAGCACCACG AAAACTAATA ACCCCGGTTC

                                BlpI
```

Fig. 14 (cont.)

```
                    StyI                                CelII
                    ~                                   ~~~~~~~~
1151  GCACCCTGGT GACGGTTAGC TCAGCGTCGA CCAAAGGTCC AAGCGTGTTT
      CGTGGGACCA CTGCCAATCG AGTCGCAGCT GGTTTCCAGG TTCGCACAAA

1201  CCGCTGGCTC CGAGCAGCAA AAGCACCAGC GGCGGCACGG CTGCCCTGGG
      GGCGACCGAG GCTCGTCGTT TTCGTGGTCG CCGCCGTGCC GACGGGACCC

1251  CTGCCTGGTT AAAGATTATT TCCCGGAACC AGTCACCGTG AGCTGGAACA
      GACGGACCAA TTTCTAATAA AGGGCCTTGG TCAGTGGCAC TCGACCTTGT

1301  GCGGGGCGCT GACCAGCGGC GTGCATACCT TTCCGGCGGT GCTGCAAAGC
      CGCCCCGCGA CTGGTCGCCG CACGTATGGA AAGGCCGCCA CGACGTTTCG

1351  AGCGGCCTGT ATAGCCTGAG CAGCGTTGTG ACCGTGCCGA GCAGCAGCTT
      TCGCCGGACA TATCGGACTC GTCGCAACAC TGGCACGGCT CGTCGTCGAA

1401  AGGCACTCAG ACCTATATTT GCAACGTGAA CCATAAACCG AGCAACACCA
      TCCGTGAGTC TGGATATAAA CGTTGCACTT GGTATTTGGC TCGTTGTGGT

                                          EcoRI
                                          ~~~~~~~
1451  AAGTGGATAA AAAAGTGGAA CCGAAAAGCG AATTCGGGGG AGGGAGCGGG
      TTCACCTATT TTTTCACCTT GGCTTTTCGC TTAAGCCCCC TCCCTCGCCC

1501  AGCGGTGATT TTGATTATGA AAAGATGGCA AACGCTAATA AGGGGGCTAT
      TCGCCACTAA AACTAATACT TTTCTACCGT TTGCGATTAT TCCCCCGATA
                                gIIIseq9  100.0%
                              ========================

1551  GACCGAAAAT GCCGATGAAA ACGCGCTACA GTCTGACGCT AAAGGCAAAC
      CTGGCTTTTA CGGCTACTTT TGCGCGATGT CAGACTGCGA TTTCCGTTTG

                                             ClaI
                                             ~~~~~~
1601  TTGATTCTGT CGCTACTGAT TACGGTGCTG CTATCGATGG TTTCATTGGT
      AACTAAGACA GCGATGACTA ATGCCACGAC GATAGCTACC AAAGTAACCA

1651  GACGTTTCCG GCCTTGCTAA TGGTAATGGT GCTACTGGTG ATTTTGCTGG
      CTGCAAAGGC CGGAACGATT ACCATTACCA CGATGACCAC TAAAACGACC

1701  CTCTAATTCC CAAATGGCTC AAGTCGGTGA CGGTGATAAT TCACCTTTAA
      GAGATTAAGG GTTTACCGAG TTCAGCCACT GCCACTATTA AGTGGAAATT

1751  TGAATAATTT CCGTCAATAT TTACCTTCCC TCCCTCAATC GGTTGAATGT
      ACTTATTAAA GGCAGTTATA AATGGAAGGG AGGGAGTTAG CCAACTTACA

1801  CGCCCTTTTG TCTTTGGCGC TGGTAAACCA TATGAATTTT CTATTGATTG
      GCGGGAAAAC AGAAACCGCG ACCATTTGGT ATACTTAAAA GATAACTAAC

1851  TGACAAAATA AACTTATTCC GTGGTGTCTT TGCGTTTCTT TTATATGTTG
      ACTGTTTTAT TTGAATAAGG CACCACAGAA ACGCAAAGAA AATATACAAC

1901  CCACCTTTAT GTATGTATTT TCTACGTTTG CTAACATACT GCGTAATAAG
      GGTGGAAATA CATACATAAA AGATGCAAAC GATTGTATGA CGCATTATTC
```

Fig. 14 (cont.)

```
                    HindIII
                    ~~~~~~
1951  GAGTCTTGAT AAGCTTGACC TGTGAAGTGA AAAATGGCGC AGATTGTGCG
      CTCAGAACTA TTCGAACTGG ACACTTCACT TTTTACCGCG TCTAACACGC
                          OGIII3  100.0%
                        ====================

2001  ACATTTTTTT TGTCTGCCGT TTAATGAAAT TGTAAACGTT AATATTTTGT
      TGTAAAAAAA ACAGACGGCA AATTACTTTA ACATTTGCAA TTATAAAACA

2051  TAAAATTCGC GTTAAATTTT TGTTAAATCA GCTCATTTTT TAACCAATAG
      ATTTTAAGCG CAATTTAAAA ACAATTTAGT CGAGTAAAAA ATTGGTTATC

2101  GCCGAAATCG GCAAAATCCC TTATAAATCA AAAGAATAGA CCGAGATAGG
      CGGCTTTAGC CGTTTTAGGG AATATTTAGT TTTCTTATCT GGCTCTATCC

2151  GTTGAGTGTT GTTCCAGTTT GGAACAAGAG TCCACTATTA AAGAACGTGG
      CAACTCACAA CAAGGTCAAA CCTTGTTCTC AGGTGATAAT TTCTTGCACC

2201  ACTCCAACGT CAAAGGGCGA AAAACCGTCT ATCAGGGCGA TGGCCCACTA
      TGAGGTTGCA GTTTCCCGCT TTTTGGCAGA TAGTCCCGCT ACCGGGTGAT

2251  CGAGAACCAT CACCCTAATC AAGTTTTTTG GGGTCGAGGT GCCGTAAAGC
      GCTCTTGGTA GTGGGATTAG TTCAAAAAAC CCCAGCTCCA CGGCATTTCG

2301  ACTAAATCGG AACCCTAAAG GGAGCCCCCG ATTTAGAGCT TGACGGGGAA
      TGATTTAGCC TTGGGATTTC CCTCGGGGGC TAAATCTCGA ACTGCCCCTT

2351  AGCCGGCGAA CGTGGCGAGA AAGGAAGGGA AGAAAGCGAA AGGAGCGGGC
      TCGGCCGCTT GCACCGCTCT TTCCTTCCCT TCTTTCGCTT TCCTCGCCCG

2401  GCTAGGGCGC TGGCAAGTGT AGCGGTCACG CTGCGCGTAA CCACCACACC
      CGATCCCGCG ACCGTTCACA TCGCCAGTGC GACGCGCATT GGTGGTGTGG

2451  CGCCGCGCTT AATGCGCCGC TACAGGGCGC GTGCTAGCCA TGTGAGCAAA
      GCGGCGCGAA TTACGCGGCG ATGTCCCGCG CACGATCGGT ACACTCGTTT

2501  AGGCCAGCAA AAGGCCAGGA ACCGTAAAAA GGCCGCGTTG CTGGCGTTTT
      TCCGGTCGTT TTCCGGTCCT TGGCATTTTT CCGGCGCAAC GACCGCAAAA

2551  TCCATAGGCT CCGCCCCCCT GACGAGCATC ACAAAAATCG ACGCTCAAGT
      AGGTATCCGA GGCGGGGGGA CTGCTCGTAG TGTTTTTAGC TGCGAGTTCA

2601  CAGAGGTGGC GAAACCCGAC AGGACTATAA AGATACCAGG CGTTTCCCCC
      GTCTCCACCG CTTTGGGCTG TCCTGATATT TCTATGGTCC GCAAAGGGGG

2651  TGGAAGCTCC CTCGTGCGCT CTCCTGTTCC GACCCTGCCG CTTACCGGAT
      ACCTTCGAGG GAGCACGCGA GAGGACAAGG CTGGGACGGC GAATGGCCTA

2701  ACCTGTCCGC CTTTCTCCCT TCGGGAAGCG TGGCGCTTTC TCATAGCTCA
      TGGACAGGCG GAAAGAGGGA AGCCCTTCGC ACCGCGAAAG AGTATCGAGT

2751  CGCTGTAGGT ATCTCAGTTC GGTGTAGGTC GTTCGCTCCA AGCTGGGCTG
      GCGACATCCA TAGAGTCAAG CCACATCCAG CAAGCGAGGT TCGACCCGAC

        ApaLI
        ~~~~~~
```

Fig. 14 (cont.)

HindIII
~~~~~~

```
1951  GAGTCTTGAT AAGCTTGACC TGTGAAGTGA AAAATGGCGC AGATTGTGCG
      CTCAGAACTA TTCGAACTGG ACACTTCACT TTTTACCGCG TCTAACACGC
                          OGIII3  100.0%
                        ====================

2001  ACATTTTTTT TGTCTGCCGT TTAATGAAAT TGTAAACGTT AATATTTTGT
      TGTAAAAAAA ACAGACGGCA AATTACTTTA ACATTTGCAA TTATAAAACA

2051  TAAAATTCGC GTTAAATTTT TGTTAAATCA GCTCATTTTT TAACCAATAG
      ATTTTAAGCG CAATTTAAAA ACAATTTAGT CGAGTAAAAA ATTGGTTATC

2101  GCCGAAATCG GCAAAATCCC TTATAAATCA AAAGAATAGA CCGAGATAGG
      CGGCTTTAGC CGTTTTAGGG AATATTTAGT TTTCTTATCT GGCTCTATCC

2151  GTTGAGTGTT GTTCCAGTTT GGAACAAGAG TCCACTATTA AAGAACGTGG
      CAACTCACAA CAAGGTCAAA CCTTGTTCTC AGGTGATAAT TTCTTGCACC

2201  ACTCCAACGT CAAAGGGCGA AAAACCGTCT ATCAGGGCGA TGGCCCACTA
      TGAGGTTGCA GTTTCCCGCT TTTTGGCAGA TAGTCCCGCT ACCGGGTGAT

2251  CGAGAACCAT CACCCTAATC AAGTTTTTTG GGGTCGAGGT GCCGTAAAGC
      GCTCTTGGTA GTGGGATTAG TTCAAAAAAC CCCAGCTCCA CGGCATTTCG

2301  ACTAAATCGG AACCCTAAAG GGAGCCCCCG ATTTAGAGCT TGACGGGGAA
      TGATTTAGCC TTGGGATTTC CCTCGGGGGC TAAATCTCGA ACTGCCCCTT

2351  AGCCGGCGAA CGTGGCGAGA AAGGAAGGGA AGAAAGCGAA AGGAGCGGGC
      TCGGCCGCTT GCACCGCTCT TTCCTTCCCT TCTTTCGCTT TCCTCGCCCG

2401  GCTAGGGCGC TGGCAAGTGT AGCGGTCACG CTGCGCGTAA CCACCACACC
      CGATCCCGCG ACCGTTCACA TCGCCAGTGC GACGCGCATT GGTGGTGTGG

2451  CGCCGCGCTT AATGCGCCGC TACAGGGCGC GTGCTAGCCA TGTGAGCAAA
      GCGGCGCGAA TTACGCGGCG ATGTCCCGCG CACGATCGGT ACACTCGTTT

2501  AGGCCAGCAA AAGGCCAGGA ACCGTAAAAA GGCCGCGTTG CTGGCGTTTT
      TCCGGTCGTT TTCCGGTCCT TGGCATTTTT CCGGCGCAAC GACCGCAAAA

2551  TCCATAGGCT CCGCCCCCCT GACGAGCATC ACAAAAATCG ACGCTCAAGT
      AGGTATCCGA GGCGGGGGGA CTGCTCGTAG TGTTTTTAGC TGCGAGTTCA

2601  CAGAGGTGGC GAAACCCGAC AGGACTATAA AGATACCAGG CGTTTCCCCC
      GTCTCCACCG CTTTGGGCTG TCCTGATATT TCTATGGTCC GCAAAGGGGG

2651  TGGAAGCTCC CTCGTGCGCT CTCCTGTTCC GACCCTGCCG CTTACCGGAT
      ACCTTCGAGG GAGCACGCGA GAGGACAAGG CTGGGACGGC GAATGGCCTA

2701  ACCTGTCCGC CTTTCTCCCT TCGGGAAGCG TGGCGCTTTC TCATAGCTCA
      TGGACAGGCG GAAAGAGGGA AGCCCTTCGC ACCGCGAAAG AGTATCGAGT

2751  CGCTGTAGGT ATCTCAGTTC GGTGTAGGTC GTTCGCTCCA AGCTGGGCTG
      GCGACATCCA TAGAGTCAAG CCACATCCAG CAAGCGAGGT TCGACCCGAC
```

ApaLI
~~~~~~

Fig. 14 (cont.)

```
2801  TGTGCACGAA CCCCCCGTTC AGTCCGACCG CTGCGCCTTA TCCGGTAACT
      ACACGTGCTT GGGGGGCAAG TCAGGCTGGC GACGCGGAAT AGGCCATTGA

2851  ATCGTCTTGA GTCCAACCCG GTAAGACACG ACTTATCGCC ACTGGCAGCA
      TAGCAGAACT CAGGTTGGGC CATTCTGTGC TGAATAGCGG TGACCGTCGT

2901  GCCACTGGTA ACAGGATTAG CAGAGCGAGG TATGTAGGCG GTGCTACAGA
      CGGTGACCAT TGTCCTAATC GTCTCGCTCC ATACATCCGC CACGATGTCT

2951  GTTCTTGAAG TGGTGGCCTA ACTACGGCTA CACTAGAAGA ACAGTATTTG
      CAAGAACTTC ACCACCGGAT TGATGCCGAT GTGATCTTCT TGTCATAAAC

3001  GTATCTGCGC TCTGCTGTAG CCAGTTACCT TCGGAAAAAG AGTTGGTAGC
      CATAGACGCG AGACGACATC GGTCAATGGA AGCCTTTTTC TCAACCATCG

3051  TCTTGATCCG GCAAACAAAC CACCGCTGGT AGCGGTGGTT TTTTTGTTTG
      AGAACTAGGC CGTTTGTTTG GTGGCGACCA TCGCCACCAA AAAAACAAAC

3101  CAAGCAGCAG ATTACGCGCA GAAAAAAAGG ATCTCAAGAA GATCCTTTGA
      GTTCGTCGTC TAATGCGCGT CTTTTTTTCC TAGAGTTCTT CTAGGAAACT

3151  TCTTTTCTAC GGGGTCTGAC GCTCAGTGGA ACGAAAACTC ACGTTAAGGG
      AGAAAAGATG CCCCAGACTG CGAGTCACCT TGCTTTTGAG TGCAATTCCC

3201  ATTTTGGTCA GATCTAGCAC CAGGCGTTTA AGGGCACCAA TAACTGCCTT
      TAAAACCAGT CTAGATCGTG GTCCGCAAAT TCCCGTGGTT ATTGACGGAA

3251  AAAAAAATTA CGCCCCGCCC TGCCACTCAT CGCAGTACTG TTGTAATTCA
      TTTTTTTAAT GCGGGGCGGG ACGGTGAGTA GCGTCATGAC AACATTAAGT

3301  TTAAGCATTC TGCCGACATG GAAGCCATCA CAAACGGCAT GATGAACCTG
      AATTCGTAAG ACGGCTGTAC CTTCGGTAGT GTTTGCCGTA CTACTTGGAC

3351  AATCGCCAGC GGCATCAGCA CCTTGTCGCC TTGCGTATAA TATTTGCCCA
      TTAGCGGTCG CCGTAGTCGT GGAACAGCGG AACGCATATT ATAAACGGGT

3401  TAGTGAAAAC GGGGGCGAAG AAGTTGTCCA TATTGGCTAC GTTTAAATCA
      ATCACTTTTG CCCCCGCTTC TTCAACAGGT ATAACCGATG CAAATTTAGT

3451  AAACTGGTGA AACTCACCCA GGGATTGGCT GAGACGAAAA ACATATTCTC
      TTTGACCACT TTGAGTGGGT CCCTAACCGA CTCTGCTTTT TGTATAAGAG

3501  AATAAACCCT TTAGGGAAAT AGGCCAGGTT TTCACCGTAA CACGCCACAT
      TTATTTGGGA AATCCCTTTA TCCGGTCCAA AAGTGGCATT GTGCGGTGTA

3551  CTTGCGAATA TATGTGTAGA AACTGCCGGA AATCGTCGTG GTATTCACTC
      GAACGCTTAT ATACACATCT TTGACGGCCT TTAGCAGCAC CATAAGTGAG

   +1
3601  CAGAGCGATG AAAACGTTTC AGTTTGCTCA TGGAAAACGG TGTAACAAGG
      GTCTCGCTAC TTTTGCAAAG TCAAACGAGT ACCTTTTGCC ACATTGTTCC

3651  GTGAACACTA TCCCATATCA CCAGCTCACC GTCTTTCATT GCCATACGGA
      CACTTGTGAT AGGGTATAGT GGTCGAGTGG CAGAAAGTAA CGGTATGCCT
```

Fig. 14 (cont.)

```
3701   ACTCCGGGTG AGCATTCATC AGGCGGGCAA GAATGTGAAT AAAGGCCGGA
       TGAGGCCCAC TCGTAAGTAG TCCGCCCGTT CTTACACTTA TTTCCGGCCT

3751   TAAAACTTGT GCTTATTTTT CTTTACGGTC TTTAAAAAGG CCGTAATATC
       ATTTTGAACA CGAATAAAAA GAAATGCCAG AAATTTTTCC GGCATTATAG

3801   CAGCTGAACG GTCTGGTTAT AGGTACATTG AGCAACTGAC TGAAATGCCT
       GTCGACTTGC CAGACCAATA TCCATGTAAC TCGTTGACTG ACTTTACGGA

3851   CAAAATGTTC TTTACGATGC CATTGGGATA TATCAACGGT GGTATATCCA
       GTTTTACAAG AAATGCTACG GTAACCCTAT ATAGTTGCCA CCATATAGGT

3901   GTGATTTTTT TCTCCATTTT AGCTTCCTTA GCTCCTGAAA ATCTCGATAA
       CACTAAAAAA AGAGGTAAAA TCGAAGGAAT CGAGGACTTT TAGAGCTATT

3951   CTCAAAAAAT ACGCCCGGTA GTGATCTTAT TTCATTATGG TGAAAGTTGG
       GAGTTTTTTA TGCGGGCCAT CACTAGAATA AAGTAATACC ACTTTCAACC

4001   AACCTCACCC GACGTCTAAT GTGAGTTAGC TCACTCATTA GGCACCCCAG
       TTGGAGTGGG CTGCAGATTA CACTCAATCG AGTGAGTAAT CCGTGGGGTC

4051   GCTTTACACT TTATGCTTCC GGCTCGTATG TTGTGTGGAA TTGTGAGCGG
       CGAAATGTGA AATACGAAGG CCGAGCATAC AACACACCTT AACACTCGCC

                  M13 Reverse  primer 100.0%
                      ==================
4101   ATAACAATTT CACACAGGAA ACAGCTATGA CCATGATTAC GAATT
       TATTGTTAAA GTGTGTCCTT TGTCGATACT GGTACTAATG CTTAA
```

Fig. 14 (cont.)